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Copyright (c) 1993 - 2000

    protein search, using sw model

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91.7 91.7	(first entry) y sel-10 prote y sel-10 prote presenilin; therapy. 970S-006824 WACIA & UPJUHN Li J, Pauley 8026/38. human sel-10 ge 60-63; 91pp
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New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug talgets in the treatment of Alzheimer's disease

PHARMACIA & UPJOHN CO

(PHAA

99US-0328877.

99-JUN-1999;

23-MAY-2000; 2000WO-US09814.

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Pauley AM,

WPI; 2001-102404

Claim 1; Page 79-82; 116pp; English.

The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assay for detecting sel-10 polypeptide expression. The sel-10 polymeptides are also useful as dritargets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polymeclectides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.

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This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human mammary sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's
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Human mammary

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Sel-10;

WO200075328-A1

14-DEC-2000

Homo sapiens

first entry)

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The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide sxpression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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 YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 559;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human sel-10 polypeptides
                                                                                                                                                             Human mammary sel-10 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 63-66; 91pp; English.
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100.0%; Pre-
0;
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                                                                                                                                                                                                                                                                                                                                                    97US-0068243.
                                                                      AAY22467 standard; Protein;
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                                                                                                                                 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX99702
                                                                                                                                                                                                      mammary gland;
                                                                                                                                                                                       Sel-10; human;
                                                                                                                                                                                                                                                               WO9932623-A1
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                        17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                    19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                               ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559;
                                                                                                   AAY22467;
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AAY22465 standard; Protein; 540
WPI; 2000-400073/34.
N-PSDB; AAA49199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baughn
                                                    FGDLRAANGQGQQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHM
                                              MOVIEPOFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEE
                                                                        GIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQ
                                                                                                   FCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNA
                                                                                                                             ETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQ
                                                                                                                                                       YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDV
                                                                                                                                                                                  ETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVT
                                                                                                                                                                                                            CLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGS
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99US-0118610.
99US-0127990.
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                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US28013
                                                                                                                                                                                                                                                                                   AAB01204 standard; Protein;
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Azimzai Y;
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                                                                                                                                                                  Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is human GTPAP-29 protein. This sequence was derived from a cDNA library of brain tumour tissue. This protein is expressed in nervous, reproductive and gastrointestinal tissue. The GTPAP proteins may be used to define agonists and antagonists of GTPAP activity and to generate antibodies to GTPAP. This means the GTPAP proteins may be useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders, atthma, inflammatory disorders, immune system disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYD 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRN 572
polynucleotides, and antibodies, and treating various diseases such immune deficiency syndrome (AIDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                          Claim 1; Page 118-120; 144pp; English
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Human GTPase associated proteins, useful for diagnosing, preventing atherosclerosis, cancer, acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.6%; Sccilarity 100.0%; Pr
Conservative 0;
                                                                           asthma, and autoimmune diseases
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WPI; 1999-458026/38
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                                                                                                                                                                                      Sel-10; human;
                                                                                                                                                                                                 gland;
                                                                                                                                                                  Human mammary
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                                                                                                                     AAY22468;
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                                          PS-1; PS-2; hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE 169
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                                         Sel-10; human; presenilin; Alzheimer's disease;
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100.0%; Pred. No. 0;
ive 0; Mismatches
                   Human hippocampal sel-10 protein sequence.
                                                                                                                                                                                                                                                           New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                               Claim 24; Page 57-59; 91pp; English
                                                                                                                                                                                   (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                      Gurney ME, Li J, Pauley AM;
                                                                                                                                                              97US-0068243.
                                                                                                                                        98WO-US26820.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 540; Conservative
(first
                                                                                                                                                                                                                            WPI; 1999-458026/38.
N-PSDB; AAX99701.
                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                        540 AA;
                                                                        Homo sapiens.
                                                                                             W09932623-A1
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29-SEP-1999
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This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human mammary sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS 109
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VQPPTGLQEWIKMFQSWSGPEKLIALDELIDSCEPTQVKHMMQVIEPQFQRDF1SLLPKE
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                                                       LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK
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                                                                                                                                                                                                                                                                                                                                                      presentlin; Alzheimer's disease; therapy.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                sel-10 protein sequence.
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MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS 109

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VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE 169

LALYYLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFI 229

HSPWKSAYIRQHRIDINWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS

349 300 360 469

HLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD 409

PETETCLHTLQGHTNRVYSLQFDG1HVVSGSLDTS1RVWDVETGNC1HTLTGHQSLTSGM

AVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM

529

ELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVK

LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to human sel-10. The sel-10 proteins
                             hspwksayirghridtnwrrgelkspkvlkghddhvitclqfcgnrivsgsddntlkvws
                                                         HLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD
                                                                                                PETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETCNCIHTLTGHQSLTSGM
                   AVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         their encoding polynucleotides, detecting sel-10 polypeptide the treatment of Alzheimer's di
                                                                                                                                                                                                                                                                                                                              Sel-10; human; Alzheimer's disease; Abeta.
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                                                                                                                                                                                                                                                                                                          Human hippocampal sel-10-5 protein
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ful for raising antibodies for
ression and as drug targets in
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New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
                                                                                          Alzheimer's disease; Abeta.
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                  Æ
                  540
                                                                        Human mammary sel-10-3 protein.
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                 AAB59200 standard; protein;
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                                  AAB59200;
                                                                                          Sel-10;
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Length 540;

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Score 540; Pred. No.

91.7%; 91.00.0%;

Match Local Similarity

Query Best L

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97US-0068243.

98WO-US26820

Pauley AM;

Li J,

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New isolated human sel-10 polypeptides
                                             (PHAA ) PHARMACIA & UPJOHN
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                                                                                        N-PSDB; AAX99701
                           19-DEC-1997;
          17-DEC-1998;
                                                              Gurney ME,
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              the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
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         invention relates to human sel-10.
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                                                                                                                        Query Match 91.7%; Score 540; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 540; Conservative 0; Mismatches
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(PS-1)
                       This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human hippocampal sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-10 PP-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                               New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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                                                                                         Sel-10; human; Alzheimer's disease; Abeta
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                                                     Human hippocampal sel-10-4 protein
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Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; hippocampus;
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Pred. No.
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avtgkclrtlvghtggvwssqmrdniiisgstdrtlkvwnaetgecihtlyghtstvrcm
                                                                                   HLHEKRVVSGSRDATLRVWDIETGOCLHVLMGHVAAVRCVOYDGRRVVSGAYDFMVKVWD
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                              AVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM
                                                                                                                                                                                                                                                                                                                                                                     Sel-10; human; Alzheimer's disease; Abeta.
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DB 22; Length 553;

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Query Match

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                                                    mkrkldhgsevrsfslgkkpckvseytsttglvpcsatpttfgdlraangggggrrrits 73
                                                                                                                            AVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM
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           Indels
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99US-0328877.

09-JUN-1999;

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       This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human hippocampal sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of
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Best Local Similarity 100.
Matches 540; Conservative
                                                                 Alzheimer's disease
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                                                                                                                                                                              the present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the blological pathways that lead to Alzheimer's disease.
                                                                                             New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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Search completed: September 25, 2001, 14:45:34

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Title: Perfect score:

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IF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REFERENCE/DOCKET NUMBER: 0575/53200/JPM/AKC
TELEPHONE: (212) 278-0400
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION SEQ ID NO: 6:
CONTRACT (212) 278-0400
TELEFORMET (212) 278-0400
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100.0%; Pred. No. 0.0016;
iive 0; Mismatches 0;
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US-08-557-142-3
US-08-557-142-3
US-08-557-142-4
PCT-US94-06264-3
PCT-US94-06264-3
PCT-US94-06264-4
US-08-862-607-5
US-08-862-607-5
US-09-203-232-324A-4
US-08-152-324A-5
US-09-203-232-324A-5
US-08-152-324A-4
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US-08-152-324A-4
US-08-152-324A-7
US-08-16144-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-468-819-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
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STATE: New York
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-671-0948-3

US-08-671-0948-5

US-08-311-3078-6

US-08-311-3078-6

US-08-311-3078-4

US-08-311-3078-4

US-08-311-3078-4

US-07-792-988-3

US-07-792-988-3

US-07-778-413E-19

US-07-778-413E-19

US-07-778-413E-19

US-08-340-102-18

US-08-340-102-18

US-08-340-102-18

US-08-330-163-3

US-08-330-163-3

US-08-330-163-3

US-08-330-163-3

US-08-340-103-103-103-0

US-08-330-163-3

US-08-340-103-103-103-0

US-08-330-163-3

US-08-340-113-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          197339 seqs, 20590346 residues
                                                                                                                                                              September 25, 2001, 14:43:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                 US-09-328-877A-8
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Query
Match Length DB
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Gaps

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APPLICATION NUMBER: US/08/671,094B
FILING DATE: 28-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INNORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REGISTRATION NUMBER: 27,643
REGISTRATION NUMBER: 63086FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
TELEPA: (215)563-4100
SEQUENCE CHARACTERISTICS:
CENGTH: 13 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08671094B
Patent No. 5912232
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 OCLOTLOG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QCLQTLQG 10
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TITLE OF INVENTION: Anti-inflammatory Polypeptide
TITLE OF INVENTION: Antagonists of Human Interleukin-8
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
CONNTRY: U.S.A.
2 ID: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24.JUL-1997
CLASSIFICATION: 435
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ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNBER: 28,678
REGISTRATION UNBER: 0575/53200/JPW/AKC
REPERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0403
TELEFAX: (212) 278-0403
TELEFAX: (212) 278-0403
TELEFAX: (312) 278-0403
TELEFAX: (312) 278-0403
TELEFAX: (312) 278-0403
TELEFAX: (312) 378-0403
TELEFAX: (312) 378-0403
TELEFAX: (312) 378-0403
TELEFAX: (312) 378-0403
TELEFAX: (313) 378-0403
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12; DB 3;
Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08671094B Patent No. 5912232 GENERAL INFORMATION:
                                                                                                     Sequence 2, Application US/08899578 Patent No. 6087153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0%; Scc
Best Local Similarity 100.0%; P.
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-899-578-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 SGSLDTSIRVWD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 SGSLDTSIRVWD 446
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US-08-671-094B-3
                                   RESULT 2
US-08-899-578-2
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NAME/KEY: Modified-site
LOCATION: 4..6
OTHER INFORMATION: /note= "The cysteine residues
OTHER INFORMATION: may be substituted with aminobutryic acid, homocysteine, o
OTHER INFORMATION: diaminosuberic acid."
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                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Talmadge, James E.
APPLICANT: Talmadge, James E.
TITLE OF INVENTION: Anti-inflammatory Polypeptide
TITLE OF INVENTION: Antagonists of Human Interleukin-8
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,094B
FILING DATE: 28-JUN-1996
CLASSIFYCATION 1514
ATTORNEY/ACENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 63086FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
TELEFAN: (215)563-4004
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FRACTH: 13 amino acids
                                                                                                                                                                                                                                   1.4%; Score 8; DB 2;
100.0%; Pred. No. 0.76;
rative 0; Mismatches
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/note= "The cysteine residues may
be substituted with aminobutyric acid, homocysteine, or
diaminosuberic acid."
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tallade, James E.
TITLE OF INVENTION: Polypeptide Agonist Derived From Human TITLE OF INVENTION: Interleukin-8 NUMBER OF SEQUENCES: 12
CORRESPONDENCE 12
ADDRESSE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                   Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Usa

2IP: 19103-2307

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,307B
FILING DATE: 23-SEP-194
ATTOMEY/AGENT INFORMATION:
NAME: Hagan, Patrick J:
REGISTRATION NUMBER: 27,643
REGISTRATION NUMBER: 27,643
REGISTRATION NUMBER: 27,643
FELECOMMUNICATION NUMBER: 63085
TELECOMMUNICATION NUMBER: 63085
TELECOMMUNICATION NUMBER: 63085
TELECOMMUNICATION NUMBER: 63085
TELEFAX: (215)563-4100
SEQUENCE CHARRACTERISTICS:
TEMATH. 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 8; DB 1;
100.0%; Pred. No. 0.86;
tive 0; Mismatches
                Score 8; DB 2;
; Pred. No. 0.81
0; Mismatches
                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08311307B Patent No. 5627156 GENERAL INFORMATION:
1.4%; Scc.
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant MOLECUE TYPE: pertide HYPOTHERICAL: NO ANTI-SENSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
        Query Match 1.4
Best Local Similarity 100.
Matches 8; Conservative
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OTHER INFORMATION:
OTHER INFORMATION: 1
OTHER INFORMATION: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                            494 OCLOTLOG 501
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US-08-311-307B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-311-307B-6
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                                                                                                                                                                                                                            /note= "The cysteine residues
may be substituted with aminobutyric acid, homocysteine, or
diaminosuberic acid."
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may be substituted with aminobutyric acid, homocysteine, or diaminosuberic acid."
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APPLICANT: Talmadge, James E.

APPLICANT: Talmadge, James E.

TITLE OF INVENTION: Anti-inflammatory Polypeptide

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street

STREET: 1601 Market Street

STREET: PA

CONFUTR: DAA

CONFUTR: DAA

CONFUTR: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BACHAIN REPRESSER: US/08/671,094B

FILING DATE: 28-JUN-1996

CLASSIFTCATION NUMBER: 27,643

RECISTRATION NUMBER: 27,643

RESPERANCE/DOCKET UNBARTION:

NAME: Hagan, Patrick J.

RESPERANCE/DOCKET UNBARTION:

TELEPHONE: (215)563-4100

TELEPHONE: (215)563-4100

TELEPHONE: ANTION INVERMATION:

TELEPHONE: ANTION AND ANTION:

TELEPHONE: ANTION ANTION ANTION:

TELEPHONE: ANTION ANTION ANTION:

TELEPHONE: ANTION ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 8; DB 2; Length 13; 100.0%; Pred. No. 0.76; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08671094B
Patent No. 5912232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
           STRANDEDNESS: not relevant
                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                    not relevant
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.4
Best Local Similarity 100.
Matches 8; Conservative
                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                    ; NAME/KEY: Modified-s; LOCATION: 4.6
; OTHER INFORMATION: //; OTHER INFORMATION: m.; CHER INFORMATION: d. US-08-671-094B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4..6
OTHER INFORMATION: ,
OTHER INFORMATION: r
OTHER INFORMATION: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 QCLQTLQG 501
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ANTI-SENSE: NO
FEATURE:
                                                                                                                 ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-671-094B-2
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GENERAL INFORMATION:

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/note= "The cysteine residues may
be substituted with aminobutyric acid, homocysteine or
diaminosuberic acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 8; DB 1; Length 16; 100.0%; Pred. No. 0.91; tive 0; Mismatches 0; Indels
                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,307B
FILING DATE: 23-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 27,643
RELEPRACION NUMBER: 27,643
RELEPRACION SECTION INFORMATION:
TELEPRACION SECTION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,498
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/476,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 4..6
COTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
US-08-311-307B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: HACKENSACK
STATE: NEW JERSEY
COUNTRY: U.S.A.
        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 QCLQTLQG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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be substituted with aminobutryic acid, homocysteine, or
dlaminosuberic acid."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
APPLICANT: Talmadge, James E.
TITLE OF INVENTION: Polypeptide Agonist Derived From Human TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08311307B
Patent No. 5627156
GENERAL INFORMATION:
APPLICANT: Talmadge, James E.
TITLE OF INVENTION: Polypeptide Agonist Derived From Human
TITLE OF INVENTION: Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDTUM TYPE: E10Ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,307B
FILING DATE: 23-SEP-1994
CLASSIFICATION NUMBER: 514
ATTORNEY/AGENT INFORMATION:
NAMME: Hagan, Patrick J.
REGISTRATION NUMBER: 63085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
TELEFARE (215)563-4100
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 8; DB 1;
100.0%; Pred. No. 0.91;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIE: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 4..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: /
; OTHER INFORMATION: b,
; OTHER INFORMATION: di
US-08-311-3078-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 QCLQTLQG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Phila
STATE: PA
                                                                                                                                                                                                                                    STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-311-307B-4
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Gaps

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RESULT 11
US-07-792-988-4
Sequence 4, Application US/07792988
Setuence 4, Application US/07792988
TITLE OF INVENTION: Suppression of megakaryoration Suppression of megakaryoration Companies of Sequences: 4
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPESSE: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Pennsylvania
STREET: Suite 419
STREET: 133 South 36th Street
CITY: Philadelphia
STREET: 135 South 36th Street
CITY: Philadelphia
STREET: 135 South 36th Street
COMPUTE: Pennsylvania
COMPUTE: Pennsylvania
COMPUTE: Pennsylvania
COMPUTE: Pennsylvania
COMPUTE: Pappla 52,6
COMPUTE: EN PS/2
COMPUTE: IBM PS/2
COMPUTE: IBM PS/2
COMPUTE: IBM PS/2
COMPUTE: 19911115
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,988
FILING DATE: 19911115
CLASSEICATION NUMBER: BAPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: TOWNER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
3.3;
                                                                                                                                                                                     APPLICALLO...
RELING DATE:
ATORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISPRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-159
TELECOMUNICATION INFORMATION:
TELEFAX: (215) 568-8383
TELEFAX: (215) 568-8383
TELEX: No. 5306709e
INFORMATION FOR SEQ ID No: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
LENGTH: 73 amino acids
"""" AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                         OPERATING SYSTEM: MS-DOS
SOCTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                   19911115
                                                                                                                   FILING DATE: 19911111
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-07-792-988-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 OCLOTLOG 501
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TELEX: NO
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Sequence 3, Application US/07792988
Sequence 3, Application US/07792988
GENERAL INFORMATION:
APPLICANT: Gewirtz, Alan M.
ITLE OF INVENTION: Suppression of megakaryo-
TITLE OF INVENTION: Cytopoiesis by macrophage inflammatory proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: JACKSON ESQ., DAVID A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 13046 CIP A2D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPRAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Pennsylvania
STREET: Suite 419
STREET: 133 South 36th Street
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                            PRICE AND DATE:

PRICE AND DATE:

APPLICATION NUMBER: US 07/240,078
FILING DATE: 02-SEP-1988
PRICE APPLICATION DATA:

APPLICATION NUMBER: US 07/104,827
FILING DATE: 02-CCT-1987
PRICE APPLICATION DATA:

APPLICATION NUMBER: US 06/766,852
FILING DATE: 16-AUG-1985
PRICE APPLICATION DATA:

APPLICATION NUMBER: US 06/14,098
FILING DATE: 07-SEP-1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICK APPLICATION DATA:
APPLICATION NUMBER: US 06/351,290
FILING DATE: 22-FEB-1982
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/299,932
FILING DATE: 08-SEP-1981
ATTORNEY/AGENT INFORMATION:
JMBER: US 08/105,105
10-AUG-1993
                                                                                       FILING DATE: 13-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/399,971
FILING DATE: 01-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4
Best Local Similarity 100.
Matches 8; Conservative
                         FILING DATE: 10-AUG-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 19104-3246
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 OCLOTLOG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-476-376-12
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Sequence 20, Application US/07778413E

Patent No. 5401651

GENERAL INFORMATION:
APPLICANT: Walz, Alfred

TITLE OF INVENTION: No. 5401651el Neutrophil

TITLE OF INVENTION: Activating Factors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: Amgen Center
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
                                                                TITLE OF INVENTION: NO. 5401651el Neutrophil TITLE OF INVENTION: Activating Factors NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8; DB 1;
Pred. No. 3.5;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (805) 499-5725 EXTENSION 4955
TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDUNG ITE:

MEDUNG ITE:

MEDUNG ITE:

COMPUTER:

PAPEL MACCINIOSH

SOFTWARE:

MICHOSOFT WORD VERSION 5.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/778,413E

FILING DATE: 16-OCT-1991

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTATION NUMBER: 31602

REFERENCE/DOCKET NUMBER: A-204

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,413E
FILLING DATE: 16-0CT-1991
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.4%; Score 8; Best Local Similarity 100.0%; Pred. No Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                     STREET: Amgen Center
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 73 amino acids
                                                Walz, Alfred
                                                                                                                                                                                                           ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-07-778-413E-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 91320-1789
                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 QCLQTLQG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
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                                                                                                                                                                                                                                                                                                      Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: CALLIDATION

ZIP: 91320-1789

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,413E
FILING DATE: 16-0CT-1991
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: COOK, RODET R:
REGISTRATION NUMBER: 31602
REFERENCE/DOCKET NUMBER: 31602
REFERENCE/OCKET NUMBER: 3-04
TELEPHONE: (805) 499-8011
TELEPHONE: (805) 499-8011
SEQUENCE CHARACTERISTICS:
LEMBATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LEMBATION FOR SEQ ID NO: 18:
TYPE: LEMBATION DATASET CONTOWN DATASET CANDON CONTOWN 
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Patent No. 5401651
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5401651el Neutrophil
TITLE OF INVENTION: Activating Factors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMAGE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
0. 3.5;
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5. 3.5;
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100.0%; Pred. No. 3.5
:ive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 3.5
Matches 8; Conservative 0; Mismatches
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US-07-778-413E-19
; Sequence 19, Application US/07778413E
; Patent No. 5401651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Amgen Center
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single stranded
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                 ; TOPOLOGY: linear
US-07-792-988-4
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Sequence 18, Application US/08340102
Sequence 18, Application US/08340102
Sequence 18. Application US/08340102
Sequence 18. Application
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5591718e1 Neutrophil
TITLE OF INVENTION: Activating Factors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center
STREET: Amgen Center
STREET: Amgen Center
CITY: Thousand Oaks
STREET: Augen Center
STREET: Augen Center
CITY: Thousand Oaks
STREET: Amgen Center
STREET: USA
COWHYTE: USA
COWHYTE: USA
COMPUTER: MGCOSOFT WORD GENER
SOFTWARE: Macintosh
SOFTWARE: Macintosh
SOFTWARE: Macintosh
APPLICATION NUMBER: 31602
FILING DATE: 15-004-1994
CLASSIFICATION: S14
ATTORREYAGENT INFORMATION:
RECESTRATION NUMBER: 31602
REFERENCE/DOCKET NUMBER: 31602
REFERENCE/DOCKET NUMBER: 31602
REFERENCE CHARACTERISTICS:
TELEFAX: (805) 499-8011
INFORMATION FOR SEG ID NO: 18:
SEQUENCE CHARACTERISTICS:
MENTER CENTER OF SEG ID NO: 18:
MENTER OF SEG ID NO: 18:
MENTER OF SEG ID NO: 18:
MENTER OF SEG ID NO: 18:
ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31602
REFERENCE/POCKET NUMBER: A-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (805) 499-5725 EXTENSION 4955
TELEFAX: (805) 499-8011
NFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 antho acids
TYPE: antho acid
TYPE: antho acid
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-07-778-413E-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 8; Conservative 0; Mismatches
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Matches 8; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-102-18
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494 QCLQTLQG 501

Search completed: September 25, 2001, 14:45:58 Job time: 138 sec

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A; Gene: CESP: F55B12.3
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GRO-gamma precurso
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hypothetical prote
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Copyright (c) 1993 - 2000 Compugen Ltd.
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A;Molecule type: DNA
A;Residues: 1-579 <WIL>
A;Cross-references: EMBL:Z79757; PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3
A;Experimental source: clone F55B12
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKF2p434G0511.1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: T46510 However, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000 A;Reference number: 233035 A;Reference number: 233035 A;Reference number: 246310 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-524 AAA>
                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T22703
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A;Rxperimental source: adult testis; clone DKFZp434G0511
C;Genetics:
A;Note: DKFZp434G0511.1
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Pred. No. 0.00071;
0; Mismatches 0;
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A;Reference number: 219602
A;Accession: T22703
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100.0%; Pred. No. 0.5
ive 0; Mismatches
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                                                T16918
S55641
S76063
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S61637
H82364
C83216
T40316
T43158
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                 A96632
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Matches 9; Conservative 0;
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Best Local Similarity 100.
Matches 12; Conservative
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Gaps

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S29121 T03288 S35208 T23179 T33915 A72737 T35570 T26943 H81932

123 135 149 164 164

190 196

hypothetical hypothetical hypothetical ypothetical hypothetical

B81173 G71430 T10221 T21783

nypothetical 1ypothetical

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melanoma growth-stimulatory activity precursor - human N;Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha; C;Species: Homo saplens (man) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999 C;Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519 R;Baker, N.E.; Kucera, G.; Richmond, A. Nucleic Acids Res. 18, 6453, 1990 A;Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) A;Reference number: S13669; MUID:91057157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rianisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chines A;Reference number: A94184; MUID:88041072
A;Reference number: A284184; MUID:88041072
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A.; Thile: IL-lalpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL A; Reference number: A60401; MUID:90187866
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A; Residues: 35-41, X', 43-49, X', 51-52, XX', 55-57 <GOL>
A; Residues: 35-41, X', 43-49, X', 1091-1100, 1990
A; Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil ntity with melanoma growth stimulatory activity.
A; Reference number: A47626; MUID:90217938
A; Accession: A47626
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A;Rosidues: 35-63,7 K',65 <SC2>
A;Rosidues: 35-63,7 K',65 <SC2>
A;Experimental source: LPS-stimulated monocytes
R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damm
J. Immunol. 150, 1000-1010, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A46519; MUID:93139489
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EMBO J. 7, 2025-2033, 1988
A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimul
A;Reference number: S00983; MUID:88328991
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A; Molecule type: protein
A; Molecule type: protein
A; Experimental Source: dermal fibroblasts
B; Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A; Title: Inflammatory cytokines induce synthesis and secretion of gro protein and A; Reference number: S03975; MUID:89246368
A; Reference number: S03976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <BAK>
A;Cross-references: EMBL:X54489; NID:934625; PIDN:CAA38361.1; PID:934626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-107 <ANI>
A;Cross-references: GB:J03561; NID:g183622; PIDN:AAA35933.1; PID:g306806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-107 <RIC>
A;Cross-references: EMBL:X12510; NID:g34621; PIDN:CAA31027.1; PID:g34622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: MG-63 osteosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4q21-4q21
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A;Residues: 35-62 <PRO>
494 OCLOTLOG 501
                                                                                 44 OCLOTIOG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S00983
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B18320
GRO-gamma precursor - human
N.Alternate names: growth-regulated protein gamma; macrophage inflammatory protein 2 B18320
C. Species: 31-May-1991 seequence_revision 27-Oct-1995 #text_change 20-Aug-1999
C. Species: 31-May-1991 seequence_revision 27-Oct-1995 #text_change 20-Aug-1999
C. Species: 31-May-1991 seequence_revision 27-Oct-1995 #text_change 20-Aug-1999
C. Arceasion: Judy28, B3820; C46519
R. Tekamp-Olson, P.; Gallegos, C. Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev, J. Exp. Med. 172, 911-919, 1990
A. Title: Cloning and characterization of CDNAs for murine macrophage inflammatory protein
A. Recense number: JH0200; MUID:90354792
A. Moccasion: JH0200; MUID:90354792
A. Moccasion: JH0200
A. MILL S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; Proc. Natl. Acad. Sci. U. S.A. 87, 7732-7736, 1990
A. Mille: Identification of three related human GRO genes encoding cytokine functions.
A. Accession: B38290
A. Molecule type: mRVA
A. Residues: 1-26, G. 29-107 CHAS
A. Residues: 1-26, G. 29-107 CHAS
A. Residues: 1-26, G. 29-107 CHAS
A. Residues: 1-28, S. Secondo A. Milley 183632; PIDN:AAA63184.1; PID:9183633
A. Molecule type: mRVA
A. Residues: 1-28, S. Secondo A. Milley 1830489
A. Molecule type: mRVA
A. Residues: 3-28 CROD
A. Title: Identification of a novel granulcyte chemotactic protein (GCP-2) from human tu A. Reperimental source: MG-63 osteosarcoma cells
A. Molecule type: protein
A. Reperimental sequence #status predicted cSIG>
B. Septimental sequence #status predicted cSIG>
F.134/Domain: signal sequence #status experimental cMA>
F.35-107/Product: GRO-gamma #status experimental cATP
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. 0.88;
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100.0%; Pred. No. 2.5;
iive 0; Mismatches
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100.0%; Pred. No. 0.8
~*** 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches B; Conserva
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318 VSGSRDATL 326
                                    357 VSGSRDATL 365
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C; Accession: $27707
R; Gullfolle, P. G.; Hutchinson, C.R.
submitted to the EMBL Data Library, August 1991
A; Description: A bacterial analog of the mdr gene of mammalian tumor cells is present
A; Reference number: $27706
                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000688; NID:g2983063; PIDN:AAC06680.1; PID:g2983073; GB:AE00
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog C,Keywords: antibiotic resistance; ATP: nucleotide binding; P-loop F;24-215/Domain: ATP-binding cassette homology <abr/>ABC><array of the control of the cassette homology <abr/>ABC><array of the control of the cassette homology <abr/>ABC><array of the control of the cassette homology <a href="https://www.edu.com/binding-motif">www.edu.com/binding-motif</a> A (P-loop)
   C;Accession: H70335
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                       Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A:Reference number: A70300; MUID:98196666
A;Accession: H70335
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Molecule type: DNA
A;Residues: 1-336 <AND>
A;Residues: 1-336 <AND>
A;Cross-references: EMBL:U21321; PIDN:AAB36970.1; GSPDB:GN00020; CESP:ZK177.6
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C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
C;Accession: T27762
R;Anderson, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces peucetius
C;Date: 07-Oct_1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001
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A;Cross-references: EMBL:M73758; NID:g153228; PIDN:AAA74717.1; PID:g153230
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                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: aq_397
C;Superfamily: Aquifex aeolicus hypothetical protein aq_397
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A;Description: The sequence of C. elegans cosmid ZK177.
A;Reference number: 220416
A;Accession: T27762
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100.0%; Pred. No. 5.7
ive 0; Mismatches
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Best Local Similarity 100.0
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-272 <AQF>
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292 EVRSFSLG 299
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A;Start codon: GTG
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A; Residues: 1-107 <HAS.
A; Cross-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629
A; Cross-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629
B; Sporn, S. A.; Elerman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskill
J. Immunol. 144, 4434-441, 1990
A; Title: Monocyte adherence results in selective induction of novel genes sharing homolo
A; Reference number: A60407; MUID:90257367
A; Accession: A60407
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: JH0281; A35931; A38290; A60407
R; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
J. Exp. Med. 172, 911-919, 1990
A; Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
A; Reference number: JH0200; MUID: 90354792
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A; Residues: 1-107 <TEK>
A; Residues: 1-107 <TEK>
A; Crotences: GB:X53799; NID:g34658; PIDN:CAA37808.1; PID:g34659
R; Iida, N.; Grotencorst, G.R.
Mol. Cell. Biol. 10, 5596-5599, 1990
A; Title: Cloning and sequencing of a new gro transcript from activated human monocytes:
A; Reference number: A35931; MUID:90377259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N'Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory C; Species: Homo sapiens (man)
C; Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
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A; Residues: 1-107 <IID>
A; Residues: 1-107 <IID>
A; Residues: 1-107 <IID>
A; Cross-references: GB M57731; GB; M36964; NID:g183626; PIDN: AAA63182.1; PID:g183627
B; Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
A; Title: Identification of three related human GRO genes encoding cytokine functions.
A; Reference number: A38290; MUID:91017578
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A.Residues: 56-107 (SPO)
C.Superfamily: beta-thromboglobulin
C.Superfamily: beta-thromboglobulin
C.Keywords: inflammation
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>
                             F;1-34/Domain: signal sequence #status predicted <SIG>F;35-107/Product: melanoma growth-stimulatory activity #status experimental <MAT>
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
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                                                                                                                                                  1.4%; Score 8; DB 2;
100.0%; Pred. No. 2.5;
tive 0; Mismatches
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100.0%; Pred. No. 2.5;
iive 0; Mismatches
C; Superfamily: beta-thromboglobulin
                                                                                                                                              Query Match 1.4
Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                494 OCLOTLOG 501
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                                                                                                                                                                                                                                                                                                                 44 QCLQTLQG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JH0281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A38290
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C; Species: Ictalurus punctatus (channel catfish)
C; Accession: I45774
R; Ngai, J; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
Cell 72, 657-666, 1993
A; Title: The family of genes encoding odorant receptors in the channel catfish.
A; Reference number: A45774; MUID:93201590
A; Reference number: A45774; MUID:93201590
A; Restaus: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: I-344 <NGA>
A; Residues: I-344 <NGA>
C; Superimental source: olfactory epithelium
A; Note: sequence extracted from NCBI backbone (NCBIP:127744)
C; Superfamily: olfactory receptor OR14
C; Keywords: olfaction; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y41C4A.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T26805
R;Steward, C.
submitted to the EMBL Data Library, October 1998
A;Accession: T26805
A;Accession: T26805
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T26805
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-386 AWIL.
A;Residues: 1-386 AWIL.
A;Residues: 1-386 AWIL.
A;Experimental source: clone Y41C4A
C;Genetics:
A;Genetics: A;Genetics: A;HO(A): 146/3; 306/3; 350/2
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A:Experimental source: strain Bristol N2; clone 2K177 C:Genetics:
A:Gene: CESP:ZK17.6
A:Map postition: 2
A:Map 175/3; 103/1; 185/3; 283/1
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100.0%; Pred. No. 7;
tive 0; Mismatches
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100.0%; Pred. No. 7.7;
tive 0; Mismatches
                                                                                                                                                                      1.4%; Score 8; DB 2;
100.0%; Pred. No. 6.9;
1ve 0; Mismatches
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Best Local Similarity 100..
Best Local 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 8; Conservative
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219 DGTVKLWD 226
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290 RIVSGSDD 297
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hypothetical protein K10B2.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 120.5ep-1999 #sequence_revision 20.5ep-1999 #text_change 20.5ep-1999
C; Accession: T16607
R; Miller, N.
Submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmid K10B2.
A; Reference number: 218545
A; Accession: T16607
A; Accession: T16607
A; Accession: T16607
A; Accession: T16607
A; Caession: T16607
A; Caession
CDC4L protein - human (fragment)
N;Alternate names: cell division control protein CDC4 homolog
C;Species: Homo Sapiens (man)
C;Date: 27-Apr-1993 #sequence_revision 26-Jul-1996 #text_change 15-Aug-1997
C;Date: 27-Apr-1993 #sequence_revision 26-Jul-1996 #text_change 15-Aug-1997
C;Accession: A43289; S30330
R;Feuchter, A.E.; Freeman, J.D.; Mager, D.L.
Genomics 13, 1237-1246, 1992
A;Title: Strategy for detecting cellular transcripts promoted by human endogenous lon A;Reference number: A43289; MUID:92372019
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hypothetical protein [imported] - Arabidopsis thaliana
hypothetical protein [imported] - Arabidopsis thaliana
(mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: A86243

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-515 STBS: BMBL:M83822
A;Cross-references: EMBL:M83822
A;Note: sequence extracted from NCBI backbone (NCBIP:111997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:K10B2.1
A;Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
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100.0%; Pred. No. 10;
ative 0; Mismatches
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100.0%; Pred. No. 13;
ative 0; Mismatches
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A;Map position: 19p13.3-19p13.3
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Best Local Similarity 100...
8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Alauthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraer, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Accession: A86243
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-821 <STO>
A; Residues: 1-821 <STO>
A; Residues: 1-821 <STO>
A; Residues: 1-821 <STO>
A; Map position: 1
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C:Species: Leishmania RNA virus 2
C:Species: Leishmania RNA virus 2
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: S56768
R:Widmer, G.; Dooley, S.
R:Widmer, G.; Dooley, G.
R:Widmer, G.; Dooley, G.
R:Widmer, G.; Dooley, G.
R:Widmer, 
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100.0%; Pred. No. 15;
Live 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 8; Conservative
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                                             treponema p
                                                                                        saccharomyc
schizosacch
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NCBI_TaxID=6239;
              P07775
P09077
                                        083647
060216
P10226
P39946
013688
P22281
P33893
P21304
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-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Sims M.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SEL-10 OR F55B12.3.
                                                                                                                                                                                                                                                                                     579 AA
                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_RGION; 1.
Repeat; WD repeat.
               BENE_ACICA
SCR_DROME
SYH_TREPA
TRN4_ECOLI
VPAP_HSV11
PACI_YEAST
CORI_SCHPO
DHAX_YEAST
GATB_YEAST
WPPI_YEAST
 YM18_PSEAE
                                                                                                                                                                RCO1_NEUCR
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WD 3.
WD 4.
WD 5.
WD 6.
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579 AA;
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Jones S.J.M.;
SE10_CAEEL
Q93794;
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(without alignments)
1885.652 Million cell updates/sec
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O46676
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Q49162
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 93435 seqs, 34255486 residues
                                                                                               September 25, 2001, 14:46:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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GBLP_SCHPO
GBB2_BOVIN
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GROA_BOVIN
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GRO_HUMAN
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MI2B_HUMAN
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DCB1_METFR
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GBB3_MOUSE
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                                                                    OM protein - protein search, using sw model
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EMBL; U95812; AAB93928.1; -.
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046676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
YOSHIMURA T., MOdi W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SWALL CYTOKINE
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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BY SIMILARITY.
94 SCD6897C21EDE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutheleostomi, Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBL_raxID-9986;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GROWTH REGULATED PROTEIN HOMOLOG GAMMA PRECURSOR (GRO-GAMMA).
; Score 12; DB 1; Leny...
...d. No. 0.0006; o' Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROZ_RABIT STANDARD; PRT; 104 AA.
P47854;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
GROWTH REGULATED PROTEIN HOWOLOG PRECURSOR (GRO HOMOLOG).
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PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
Cytokine; Growth factor; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR001089; -.
InterPro; IPR001811; -.
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                                   2.0%;
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                               Query Match 2.0
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                438 SGSLDTSIRVWD 449
                                                                                                                                       427 SGSLDTSIRVWD 438
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID 9913;
                                                                                                                                                                                                                                                         GROG_BOVIN
046675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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GRO2_RABIT
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                                                                                                                           Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A ROLE IN MONOCYTE ADHESION TO THE ENDOTHELIUM.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
YOSHIMITA T., MOGI W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH REGULATED PROTEIN HOMOLOG. BY SIMILARITY.
SEQUENCE FROM N.A. Schwartz D., Chaverri-Alamada L., Berliner J., Kirchgessner T. Gulsomoro D., Fang J., Tekamp-Olson P., Lusis J., Fogelman A., Territo M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GROWTH REGULATED PROTEIN HOMOLOG ALPHA PRECURSOR (GRO-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
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PRINTS; PR00436; INTERLEDKINB.
PRINTS; PR00437; SMALLCYTKCXC.
PROSITE; PS00471; SMALLCYTOKINES_CXC; 1.
Cytokine; Growth factor; Inflammatory response; Signal.
31 PROBABLE.
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Mismatches
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Best Local Similarity
''has 8; Conserv?
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48

1111111 41 QCLQTLQG

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InterPro; IPR001089; -. InterPro; IPR001811; -.

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Homo sapiens (Human)
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                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                   GRO_HUMAN
                                                                       GRO_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshimura T., Modi W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).
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                                                                                                                      GROWTH REGULATED PROTEIN HOMOLOG ALPHA.
BY SIMILARITY.
1002CACG64DB1F76 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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15-DEC-1998 (Rel. 37, Last annotation update)
GROWTH REGULATED PROTEIN HOMOLOG BETA PRECURSOR (GRO-BETA).
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PRINTS; PRO0437; SMALLCYTKCXC.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
Cytokine; Growth factor; Inflammatory response; Signal.
                                                  PRINTS; PRO0436; INTERLEUKINB.
PRINTS; PRO0437; SMALLCYTKCXC.
PROSITE; PSO0471; SMALL_CYTOKINES_CXC; 1.
CYtokine; Growth factor; Inflammatory response; Signal.
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100.0%; Pred. No. 1.
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0; Mismatches
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                      InterPro; IPR002473; - Pfam; PF00048; ILB; 1.
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NCBI_TaxID=9913;
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Pfam; PF00048; IL8;
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Best Local Similarity
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                                                                                                                                                                                                                                                              494 QCLQTLQG 501
                                                                                                                                                                                                                                                                               41 QCLQTLQG 48
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046677;
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494 QCLQTLQG 501

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SEQUENCE OF 35-57.

MEDLINE-89246368; PubMed=2655583;
Golds E.E., Mason P., Nyirkos P.;
Inflammatory cytokines induce synthesis and secretion of gro protein and a neutrophil chemotactic factor but not beta 2-microglobulin in human synovial cells and fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-89335650; PubMed-2670560;
Wen D., Rowland A., Derynck R.;
"Expression and secretion of gro/MGSA by stimulated human endothelial
                                                                                                                                                                                                                                                                                                                                                                                                           Richmond A., Balentien E., Thomas H.G., Flaggs G., Barton D.E., Spiess J., Bordoni R., Francke U., Derynck R.; "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin."; EMBO J. 7:2025-2033(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90217938; PubMed=2182761; Schroeder J. -M., Persoon N.L.M., Christophers E.; Schroeder J. -M., Persoon N.L.M., Christophers E.; Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil-activating peptide 1/interleukin 8, a second neutrophil-activating protein. NR2-terminal amino acid sequence identity with melanoma growth stimulatory activity."; J. Exp. Med. 171:1091-1100(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fairbrother W.J., Reilly D., Colby T., Horuk R.;
"IH assignment and secondary structure determination of human melanoma growth stimulating activity (MGSA) by NMR spectroscopy.";
FEBS Lett. 330:302-306(1993).
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-OGT-2000 (Rel. 40, Last annotation update)
GROWTH REGULATED PROTEIN PRECURSOR (MELANOMA GROWTH STIMULATORY
ACTIVITY) (MGSA) (NEUTROPHIL-ACTIVATING PROTEIN 3) (NAP-3).
SCYBI OR GROI OR GROA OR GRO OR MGSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker N.E., Kucera G., Richmond A.;
"Nucleotide sequence of the human melanoma growth stimulatory
activity (MGSA) gene.";
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-88041072; Pubmed-2890161;
Anisowicz A., Bardwell L., Sager R.;
"Constitutive overexpression of a growth-regulated gene in transformed Chinese hamster and human cells.";
Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 18:6453-6453(1990).
PRT;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=88328991; PubMed=2970963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE-93387459; Pubmed-8397104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91057157; PubMed=2129556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 8:1761-1766(1989).
 STANDARD;
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Eukaryota;
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P19875; OSUPB8;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA PRECURSOR (MIP2-ALPHA) (GROWTH REGULATED PROTEIN BETA) (GRO-BETA).
HOMO sapiens (Human).
                                                                                                                                                                             SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00048; ILB; 1.
PRINTS: PR00436; INTERLEBERINS.
PRINTS: PR00437; SMALLCYTRCAC.
PROSTIE: PS00471; SMALL_CYTOKINES.CXC; 1.
Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
                                                                                                Kim K.S., Clark-Lewis I., Sykes B.D.;
"Solution structure of GRO/melanoma growth stimulatory activity
determined by 14 NMR spectroscopy.";
J. Biol. Chem. 269:32909-32915(1994).
-!- FUNCTION: HAS CHENOTACTIC ACTIVITY FOR NEUTROPHILS. MAY PLAY A
ROLE IN INFLAMMATION AND EXERTS ITS EFFECTS ON ENDOTHELIAL CELLS
IN AN AUTOCRINE FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                    MEDLINE-94376296; PubMed-8089846; Estibrother W.J., Relly D., Colby T., Hesselgesser J., Horuk R.; "The solution structure of melanoma growth stimulating activity."; J. Mol. Biol. 242:252-270(1994).
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100.0%; Pred. No. 1.5;
ive 0; Mismatches
                                                                                      MEDLINE-95105175; PubMed-7806518;
                                                                                                                                                                                                                                                                                                   EMBL, J03561, AAA35933.1; --
EMBL, X12510; CAA31077.1; --
EMBL, X54489; CAA38361.1; --
PIR, A28414, A28414.
PIR, S00983, S00983.
PIR, S03976, S03976.
PIR, S13669, S13669.
PDB, IMGS, 30-SEP-94.
PDB, IMGS, 31-MAR-95.
                                                                                                                                                                                          C-X-C) (CHEMOKINE CXC).
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MIM; 155730; -.
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Best Local Similarity
Matches 8; Conserv
                                                                          STRUCTURE BY NMR.
           STRUCTURE BY NMR.
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MI2A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-x-C) (CHEMOKINE CXC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lida N., Grotendorst G.R.;
"Cloning and sequencing of a new gro transcript from activated human
monocytes: expression in leukocytes and wound tissue.";
Mol. Cell. Biol. 10:5596-5599(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE-91.01578; PubMed-2217207;
Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
Sanith T., Martin G., Ralph P., Sager R.;
"Identification of three related human GRO genes encoding cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMIS: PF00048; ILB; 1.
PRIMIS: PR00436; INVERLEDKINB.
PRIMIS: PR00437; SMALLCTYRCXC.
PROSTIE; PS00411; SMALL_CYTOKINES_CXC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2006939; PUDMed-10600366; Qian Y.Q., Johanson K.O., McDevitt P.; Muclear magnetic resonance solution structure of truncated human GRObeta [5-73] and its structural comparison with CXC chemokine family members GROalpha and IL-8."; J. Mol. Bloi. 294:1065-1072[1999].

-1- FUNCTION: PRODUCED BY ACTIVATED MONOCYTES AND NEUTROPHILS AND EXPRESSED AT SITES OF INFLAMMATION.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Prímates; Catarrhini; Hominidae; Homo.
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2-ALPHA.
                                                                                                                                                                                                                                                                                      macrophage
                                                                                                                SEQUENCE FROM N.A.
TISSUE-Histiocytic lymphoma;
MEDLINE-90354792; PubMed-2201751;
Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jang J.S., Kim B.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11389 MW; 740F277E928571BA CRC64;
                                                                                                                                                                                                                                                Fabre M., van Deventer S., Cerami A.;
"Cloning and characterization of cDNAs for murine
Inflammatory protein 2 and its human homologues.";
J. Exp. Med. 172:911-919(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-90377259; Pubmed-2078213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF043340, AAC03540.1; -. PIR, JH0281, JH0281.
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STRUCTURE BY NMR OF 39-107
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45
107 AA;
                                                      NCBI_TaxID=9606;
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15-JUL-1998 (Rel. 36, Created)
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P32010;
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Q09990;
                  CONFLICT
DISULFID
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YSS1_CAEEL
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-!- FUNCTION: MAY PLAY A ROLE IN INFLAMMATION AND EXERT ITS EFFECTS
ON ENDOTHELIAL CELLS IN AN AUTOCRINE FASHION.

-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (GROWTH
REGULATED PROTEIN GAMMA) (GRO-GAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91017578; PubMed-2217207;
MEDLINE-91017578; PubMed-2217207;
Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W., Smith T., Martin G., Ralph P., Sager R.;
"Identification of three related human GRO genes encoding cytokine
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=90354792; PubMed=2201751;
Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B., Fabre M., van Deventer S., Cerami A.;
"Cloning and characterization of cDNAs for murine macrophage inflammatory protein 2 and its human homologues.";
J. Exp. Med. 172:911-919(1990).
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                                       Length 107;
                                                                              0; Indels
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                                  DB 1;
. 1.5;
                                                                                                                                                                                                                                                                                  107 AA
                                                                              Mismatches
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0436; INTERLEUKINB.
PRINTS; PRO0437; SMALLCYTKCXC.
PROSITE; PSO0471; SMALL_CYTOKINES_CXC; 1.
                                  1.4%; Score 8; I
100.0%; Pred. No.
ative 0; Mismatch
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         Ouery Match
Best Local Similarity luu...
8; Conservative
                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GRO3 OR GROG.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                     494 QCLQTLQG 501
                                                                                                                                                                 44 OCLOTIOG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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MIM; 139111;
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-!- FUNCTION: DRRA AND DRRB MAY ACT JOINTLY TO CONFER DAUNORUBICIN AND DOXORUBICIN RESISTANCE BY AN EXPORT MEHANISM.
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDINE-2920801; PubMed-1924314;
Guilfoile P.G., Hutchinson C.R.;
"A bacterial analog of the mdr gene of mammalian tumor cells is present in Streptomyces peucetius, the producer of daunorubicin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces.
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                                                                                                                    Length 107;
                                                                                                                                                                 0; Indels
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                       A -> G (IN REF. 2).
97A69946B7F1F070 CRC64;
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582D66C90D54E6B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S27707; S27707.
InterPro; IPR001617; -
Pfam; PF00005; ABC_tran; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport; Antibiotic resistance.
                                                                                                                  DB 1;
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    BY SIMILARITY.
AA -> G (IN RE
                                                                                                                                                                 Mismatches
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                                                                                                                    Score 8; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 8;
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100.0%; Prec
85 BY
28 AV
11342 MW;
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                                                                                                           Query Match 1.4
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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45
27
107 AA;
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                                                                                                                                                                                                          494 QCLQTLQG 501
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292 EVRSFSLG 299
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SEQUENCE FROM N.A.
Hase T., Kimatsa Y., Yonekura K., Matsumura T., Sakakibara H.;
"Molecular cloning and differential expression of the maize ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Physiol. 96:77-83(1991).
-!- FUNCTION: FERREDOXING ARE IRON-SULFUR PROTEINS THAT TRANSFER
ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
-!- COFACTOR: BINDS A 2FE-2S CLUSTER.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1445 1715 BEACH.
1817 1859 WD 2.
182 1905 WD 3.
1918 AA; 213598 MW; 427EA619BDF9A724 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSOUGF8; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; FALSE_NEG.
PROSITE; PS50294; WD_REPEATS_REGION; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
10-AUG-1992 (Rel. 23, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
FERREDOXIN V PRECURSOR (FD V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 8; DB 1;
100.0%; Pred. No. 19;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M83822; AAB09603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001680; -.
Pfam; PF00400; WD40; 2.
PROSITE; PS50197; BEACH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1715
1859
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Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 SGSRDATL 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene family.";
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P27789;
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DOMAIN
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FER5_MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 80.3 KDA TRP-ASP REPEATS CONTAINING PROTEIN K10B2.1 IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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MD 3.

MD 4.

MD 5.

MD 6.

MD 7.

MD 8.

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MD 8.

MD 9.

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MD 1.

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Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS)
-1- SIMILARITY: STRONG, TO X.LAEVIS BETA-TRCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CDG4-LIKE PROTEIN (BEIGE-LIKE PROTEIN) (FRAGMENT).
CDC4L OR BGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1918 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0320; GPRO, PROSTER, PRO0320; GPRO, 1.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_RECION; 1.
HYPOTHETICAL protein; Repeat; WD_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WD 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U28730; AAA68258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; K10B2.1; CE02008.
InterPro; IPR001680; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
324
364
407
                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00400; WD40; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508
606
701 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                STRAIN BRISTOL N2; Miller N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                  CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC4H_HUMAN
P50851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                       K10B2.1
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CC4H_HUNAN
LC F50811
DC D1-OCT
DT 01-OCT
DE CDC4-L
DE CD
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Gaps

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Indels

Length 1918;

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HSSP; P13051;
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                                                                                                                                                        UNG_HSVE2
P53765;
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SEQUENCE
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GBLP_SCHPO
                                                                                                                                 RESULT 14
UNG_HSVE2
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            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: NICKEL ION.
-!- SUBUNIT: HOMOTETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
-!- MISCELLANEOUS: OPTIMUM ACTIVITY IS MEASURED BETWEEN PH 8 AND 9.
-!- SIMILARITY: TO M.SOEHNGENII CARBON MONOXIDE DEHYDROGENASE.
                                                                                                                                                                          FERREDOXIN V.
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
8FA43C41AD4CB976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eggen R.I.L., van Kranenburg R., Vriesema A.J.M., Geerling A.C.M., Verhagen M.F.J.M., Hagen W.R., de Vos W.M.;

"Carbon monoxide dehydrogenase from Methanosarcina frisia Gol.

Characterization of the enzyme and the regulated expression of two operon-like cdh gene clusters."

J. Biol. Chem. 271:14256-14263(1996).
 and for
                                         Maizebb; 66392; --
InterPro; IPR000564; -.
InterPro; IPR001041; -.
Pfam; PF00111; fer2; 1.
PRINTS; PR00159; ZEEZSERBOXIN.
PROSTIE; PS00197; ZEEZS_EBRREDOXIN; 1.
Electron transport; Iron-sulfur; Chloroplast; Transit peptide; Multigene family. 1.
TRANITT 1.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE I BETA SUBUNIT (EC 1.2.99.2).
                                                                                                                                                                                                                                                                       1.2%; Score 7; DB 1; Length 135; 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                  Indels
  Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74B309E6487E3E79 CRC64;
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modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      170 AA
                                                                                                                                                                                                                                                                             100.0%; Pred. ... 0; Mismatches
          entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GOE1;
MEDLINE=96278885; PubMed=8662887;
                                                                                                                                                                                                                                      MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Nickel.
SEQUENCE 170 AA; 18696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L26487; AAC37045.1; -.
                                                                                                                                                                                                                                      14399
                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanosarcina frisia.
                                                                                                                                                                                                                                     135 AA;
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                                                                                                                                                                                                                                                                                                                     436 WYSGSLD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2212;
                                                                                                                                                                                                                                                                                                                                     89 WSGSLD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCEPTOR.
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                                                                                                                                                                                                                                     SEQUENCE
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DCB1_METFR
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95302501; Pubmed-7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995).
-i- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARISE
AS A RESULT OF MISINCORPORATION OF DUMP RESIDUES BY DNA
POLYMERASE OR DUE TO DEAMINATION OF CYTOSINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL BASE (BY SIMILARITY).
20104402C5297336 CRC64;
                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equine herpesvirus type 2 (strain 86/87) (EHV-2).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                          ö
                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-UL-1998 (Rel. 36, Last annotation update)
URACIL-DNA GLYCOSYLASE (EC 3.2.2.-) (UDG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
: 33;
                             DB 1;
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100.0%; Pred. No: ...
0; Mismatches
                                                                                                                                                                                                                                                                                            255 AA
                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@lsb-sib.ch).
1.2%; Score 7; F
Pred. No.
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                                                                                                                                                                                                                                                                                               PRT;
                             100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U20824; AAC13834.1; -.
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Best Local Similarity الاس.
ناب 7; Conservative
                      Query Match 1.2
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002043; -. Pfam; PF00315; UNG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=82831;
                                                                                                                       134 ALDELID 140
                                                                                                                                                   162 ALDELID 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 CEPTQVK 148
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77 CEPTOVK 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:PK 43;
Yoshioka S., Kato K., Okayama H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                             STRAIN-972;
Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  Park S.K., Yoo H.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> A (IN REF. 2).
-> D (IN REF. 2).
4E14707164E68ACD CRC64;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L37885; AAA56865.1; --
EMBL; 299531; CAB11079.1; --
EMBL; D89247; BAA13908.1; --
Interpro; IPR001680; --
Pfam; PF00400; WD40; 7.
PRINYS; PR00320; GPROTEINBRPT.
PROSITE; PS500678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WD 2. WD 2. WD 3. WD 3. WD 5. WD 5. WD 6. WD 6. WD 6. WD 6. WD 7. 
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Gaps ö Length 314; 0; Indels 1.2%; Score 7; DB 1; 100.0%; Pred. No. 39; :Ive 0; Mismatches Query Match 1.2 Best Local Similarity 100. Matches 7; Conservative 356 VVSGSRD 362 ð

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120 VVSGSRD 126

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Search completed: September 25, 2001, 14:49:27 Job time: 206 sec

OM protein

Run on:

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09psjl ictalurus p
09xwa cenorhabdi
09yaj7 drosophila
099661 caenorhabdi
0976j3 drosophila
09gnn6 caenorhabdi
09gnn6 caenorhabdi
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Q9ese1 mus musculu
Q83070 leishmania
Q83098 leishmania
Q9ei2 human immun
Q3534 rhizobium 1
Q6651 chlorobium
Q46466 chlorobium
Q21091 caenorhabdi
Q9wx4 pseudomonas
Q06784 haematobia
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A ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

I Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagano S., Adotsuka S., Yoshikawa Y.,

Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

A Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

A Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

EMBC human cDNA sequencing project.";

EMBL; AK001933; BAA91986.1;

InterPro; IPR001880;

Pfam; PF00400; WD40; 7.

Pfam; PF00400; WD40; 7.

PROSITE; PS00181; FBOX; 1.

PROSITE; PS00181; FBOX; 1.

PROSITE; PS00181; FBOX; 1.

PROSITE; PS00181; FBOX; 1.

RWART; SM00256; PBOX; 1.

W Repeat; WD repeat.

W Repeat; WD repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTFFGDLRAANGGGOORRRITS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
CDNAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ11071 FIS, CLONE PLACE1004937, MODERATELY SIMILAR TO SEL-10
  O9h2u3 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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P72020
09gv52
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100.0%; Pred. No. 0;
.ive 0; Mismatches 0; Indels
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Q9H2U3
Q9X8U3
Q9X8U3
Q9VG17
Q9VG5
Q9G5
Q9G8D4
Q9ESE1
Q9ESE1
Q9ESE2
Q9ESE1
Q8307
Q8307
Q8307
Q61621
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  Query Match
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044083 caenorhabdi
075938 homo sapien
09520 homo sapien
099611 homo sapien
09wm9 mus musculu
Q9hsul homo sapien
Q9hsy3 nomo sapien
Q9lsy3 arabidopsis
Q9lsm8 homo sapien
                                                                                                                                                                         (without alignments)
3475.810 Million cell updates/sec
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                                                                                                                                                  ; Search time 22.42 Seconds
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Q9epn1 mus n
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                                           Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potal number of hits satisfying chosen parameters:
                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                             425026 seqs, 132305027 residues
                                                                                                                                                September 25, 2001, 14:45:36
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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Q44083
Q75938
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Q9VXP8
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sp_vertebrate:*
sp_virus:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum DB seq length: 200000000
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: sp_archea:*
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streptomyce

caenorhabdi methanosarc drosophila

Word size :

Searched:

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Result

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Gaps

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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R. Adams M.D., Celniker S.E., Holf R.A.,
R. Adams M.D., Celniker S.E., Holf R.A.,
R. Gocayer R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Bliklus G.L.G.,
R. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Berts S. D., Botchan M.R., Bulck J., Brotkstehn P., Brottler P.,
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Goler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Netchum K.A.,
R. Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
R. Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
R. Manmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469
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                                     409
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110 VOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE 169
                                                                                                                                                                                                                                                                                                      410 PETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGM
                                                                                                                                  LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFI
                                                                                                                                                                                                                                                                       HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS
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Last sequence update)
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CG15010 Drosophila melanogaster (Fruit fly).
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MEDLINE-20196006; Pubmed-10731132;
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Amerialow G., Milshina N.V., McDarry C., Mcris J., Moshrefi A.,
McMillow G., Milshina N.V., McDarry C., Mcris J., Moshrefi A.,
McMount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Amount S.M., McMan G.S., Pan S., Pollard J., Purl V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Sher E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Sylex E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ya J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
FlyBase: Fagno05556; CG15010.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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EMBL; AF020788; AAC47809.1; -.
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Last sequence update)
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InterPro; IPR001810; -.
Pfam: PF00400; WD40; 7.
Pfam: PF004646; F-box; 1.
PRINTS: PR00320; GPROTEINBRPT.
PROSITE: PS00890; ABC2_MEMBRANE; UNKNOWN_1.
PROSITE: PS00678; WD_REPEATS; UNKNOWN_5.
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Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FB0X; 1.
PROSITE; PS00678; WD_REPEATS; 5.
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(TrEMBLrel. 06, I
(TrEMBLrel. 16, 1
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Matches 21; Conservative
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587 AA;
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01-JUN-1998 (
01-MAR-2001 (
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SEQUENCE
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PROSITE; PS50197; BEACH; 1. SMART; SM00320; WD40; 1.
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Pfam; PF02138; Beach; 1.
                                                                                                                                                                                                                                                                                                        523 SDDGTVKLWD 532
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313 VSGSRDATL 321
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Neubauer G., King A., Rappsilber J., Calvio C., Watson M., Ajuh P., Sleeman J., Lamond A., Mann M.;
"Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex.";
Nat. Genet. 20:46-50(1998).
EMBL; AF083381, AAC64084.1;
Interpro; IPR001666.
Pfam; PF00400; WD40: 6.
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).

Homo sapiens (Human).

Homosi, Metazoa; (Chordata; Craniata; Vertebrata; Euteleostomi;

Hommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DB 5; Length 587;
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hes 0; Indels
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                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HOMD carriers.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
US SNRNP-SPECIFIC 40 KDA PROTEIN.
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PROSITE; PS000339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00078; WD_REPEATS; UNKNOWN_5.
SMART; SM00320; WD40; 1.
                                                                                                                                                                                                                                       310 AA.
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2.0%; Score 12; DB 100.0%; Pred. No. 0.0
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1.7%; Score 10; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 10; Conservative 0; Mismatches
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Mol. Cell. Biol. 18:6756-6766(1998).
EMBL; AF090988; AAC69625.1; -.
InterPro; IPR001680; -.
                                                                                                                                                                                                                                       PRT;
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                      Best Local Similarity 100.
Matches 12; Conservative
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                                                                                  438 SGSLDTSIRVWD 449
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  Query Match
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075938;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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Barbosa M.D.F.S., McIdde R., Kingsmore S.F.;
Identification of LYST2, a brain-specific member of the Chediak-
Higashi syndrome gene family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AROT2311, AAD41633.1;
InterPro; IPR004699;
InterPro; IPR001680;
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Sukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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InterPro; IPR002106; -.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPRCTEINBRPT.
PROSITE; PS00039; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_5.
SMART; SM00320; WD40; 1.
Repeat; WD repeat.
SEQUENCE 357 AA; 39298 MW; 87A265539437BD86 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
NFPOTHETICAL 58.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagal K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Vamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; "NBDD human cDNA sequencing project."; "Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AK022048; BAB14222.1; "NON_TER
ьикагуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_тахID=9606;
                                                                                                                                                                                                                           SEQUENCE 741 AA; 82214 MW; 8BE2038217996D07 CRC64;
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Best Local Similarity
9; Conserve
                                                                  SEQUENCE FROM N.A.
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01-MRR-2001 (TrEMBLrel. 16, Created)
01-MRR-2001 (TrEMBLrel. 16, Last sequence update)
01-MRR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12686 FIS, CLONE NT2RM4002527, WEAKLY SIMILAR TO VEGETATIBLE
INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT).
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                                         Mewes H.W., Gassenhuber J., Wiemann S.; EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tchernev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S.,
Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;
Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;
Identification of LYST2, a brain-specific member of the Chediak-Higashi syndrome gene family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF072372; AAD41634.1;
InterPro: IPR001680;
InterPro: IPR001680;
Pfam; PF02198; Beach;
Pfam; PF02138; Beach;
PROSITE; PS50197; BEACH;
PROSITE; PS50197; BEACH;
SMART; SM00320; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                       Duesterhoeff A., Lauber J., Mewes H.W., Gassenhuber J., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL, AL137748; CAB70903.1; -.
InterPro; IPR000409; -.
Pfam; PF00400; WD40; 5.
Pfam; PF02138; Beach; 2.
PROSTE; PS02139; BEACH; 1.
Hypothetical protein.
SEQUENCE 524 AA; 58801 MW; F4A38C3EFE58D390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6776B57B1D972127 CRC64;
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                                                                                                                                                                                                  DB 4;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                  SEQUENCE FROM N.A.
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SEQUENCE
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                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantue; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Length 741;
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                                            Indels
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5 AA; 94353 MW; EB5AADEDFD16F316 CRC64;
                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Pred. No. 3.3;
0; Mismatches
1.5%; Score 9; DB 4;
100.0%; Pred. No. 2.9;
             100.0%; Pred. ....
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_2.
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100.0%; Pre
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EMBL; AP000413; BAB02165.1;
InterPro; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001680; -. Pfam; PF00069; pkinase; 1. Pfam; PF00400; WD40; 7.
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ATP-binding; Repeat; Trans
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Best Local Similarity 100.
Matches 9; Conservative
                                               Conservative
                                                                                                                                                                                                                                                PRELIMINARY;
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DNA Res. 7:217-221(
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                                                                                         521 TSSDDGTVK 529
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SEQUENCE FROM N.A.
                                                                                                                STRAIN-COLUMBIA;
PubMed-10907853;
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2931 AA.

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Wang X., Herberg F.W., Laue M.M., Wullner C., Hu B.,
Petrasch-Parwez E., Kilimann M.W.;
"Neurobeachin: A protein kinase A-anchoring, beige/Chediak-Higashi
protein homolog implicated in neuronal membrane traffic.";
D. Neurosci. 20:8551-8565(2000).
EMBL; Y18276; CAC18813.1: -
SEQUENCE 29:31 AA; 326149 WW; B2E2E8E87E6B2696 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X., Herberg F.W., Laue M.M., Wullner C., Hu B., Petrasch-Parwez E., Kilimann M.W.;
"Neurobeachin: A protein kinase A-anchoring, beige/Chediak-Higashi protein homolog implicated in neuronal membrane traffic.";
J. Neurosci. 20:851-8567(2000).
EMBL; Y18276; CAC18811.1; -.
SEQUENCE 2936 AA; 326738 MW; A6CFD90CA666CEA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                          Last sequence update)
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tive 0; Mismatches
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Matches 9; Conservative
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Best Local Similarity
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PubMed=11102458;
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Petrasch-tarwaz B., Kilimann M.W.;
"Neurobeachin: A protein kinase A-anchoring, beige/Chediak-Higashi
protein homolog implicated in neuronal membrane traffic.";
J. Neurosci. 201851-8855(2000).
EMBL; Y10875; CAC18812.1; --
SEQUENCE 2904 AA; 323198 WW; B41D4ADF71AD6FF4 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA1544 PROTEIN (FRAGMENT).
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Last annotation update)
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100.0%; Pred. No. 3.9
ative 0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                      PRELIMINARY;
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Best Local Similarity
Lange 9; Conservē
SEQUENCE FROM N.A.
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TISSUE=BRAIN;
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SEQUENCE
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2936 AA

PRT;

Length 2931; Indels

DB 11;

Pred. No. 10;

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1.5%; Score 9; DB 11; Length 2936; 100.0%; Pred. No. 10; ative 0; Mismatches 0; Indels
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The SEQUENCE FROM N.A.

The Canan D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,

The complete genome of the hyperthermophilic bacterium Aquifex

RT acoliuus...

REMBL, AE000688 AAC06880.1; -.

REMBL, RE000688 AAC06880.1; -.

REMBL, SEQUENCE 272 AA: 31561 MW; 652D06C62E15D581 CRC64;
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1.4%; Score 8; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels
066716 PRELIMINARY; PRT; 272 AA. 066716; 01-AuG-1998 (TrEMBLrel. 07, Created) 01-AuG-1998 (TrEMBLrel. 07, Last sequence update) 01-AuG-1998 (TrEMBLrel. 13, Last annotation update) HYPOTHETICAL 31.6 KDA PROTEIN.
                                                                                                     AQ_397.
Aquifex aeolicus.
Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID:63363;
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Gaps .; 0

Search completed: September 25, 2001, 14:49:07 Job time: 211 sec

407 VWDPETET 414

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// Search time 20.43 Seconds
(without alignments)
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

RESULT

presenilin; Alzheimer's disease; PS-1; PS-2; therapy. New isolated human sel-10 polypeptides ry sel-10 protein sequence. Claim 24; Page 60-63; 91pp; English. standard; Protein; 589 AA. Pauley AM; (РНАА) РНАКМАСІА 6 ПРЈОНИ 改 98WO-USX6820. 97US-00682**4**\ (first entry) WPI; 1999-458026/38. N-PSDB; AAX99702. Li J, gland W09932623-A1. 19-DEC-1997; Homo sapiens 17-DEC-1998; huma 01-JUL-1999. 29-SEP-1909 Gurney ME, Нитап татт AAY22466 Sel-10; маммагу AAY2246 AAY22466

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This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human mammary sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's
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Pred. No. 1.1e-298;
Mismatches 0;
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                                                                                                                                                                                                                            The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for develophing assays for identifying agents capable of interfering with the blological pathways that lead to Alzheimer's disease.
                                                                                                                                      New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human mammary sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mammary sel-10 protein sequence.
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N-PSDB; AAX99702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human;
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and treating various diseases such as
immune deficiency syndrome (AIDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated proteins (GPRAP). The present sequence is human GTPAP-29 protein. This sequence was derived from a cDNA library of brain tumour tissue. This protein is expressed in nervous, reproductive and gastrointestinal Lissue. The GTPAP proteins may be used to define agonists and antagonists of GTPAP proteins may be useful for treatment or GTPAP. This means the GTPAP proteins may be useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders, inflammatory disorders, immune system disorders, cancer, ALDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis.
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                                                                                                                                                                                                                         Guanine nucleotide binding protein; GTP-binding protein; G-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA libraries from various tissues were screened for GTPase
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541 nlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdmk 589
                                                                                                                                                                                                                                                                                              arthritis; systemic lupus erythematosus; psoriasis; human
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Pred. No. 2.2e-298;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 118-120; 144pp; English.
                                                                                       AA.
                                                                                                                                                                                           Human GTPase associated protein-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for diagnosing, preventing atherosclerosis, cancer, acquired asthma, and autoimmune diseases -
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                                                                                   AAB01204 standard; Protein; 589
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99.8%;
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Best Local Similarity 99.8
Matches 588; Conservative
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Azimzai Y;
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                            Score 2983; DB 20;
Pred. No. 4.6e-283;
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The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                            their encoding polynucleotides, detecting sel-10 polypeptide the treatment of Alzheimer's disease
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Pred. No. 4.6e-283;
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The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
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detecting sel-10 polypeptide
the treatment of Alzheimer's disease
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                  VSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCI
                                                                                                                               NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE
                                                               HTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK
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                                                                                                                                                                                                             577 TKLLVLDFDVDMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2000;
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hes 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human hippocampal sel-10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of
                                                                                          Sel-10; human; presentlin; Alzheimer's disease; PS-1; PS-2; hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156
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20 llpvllpn----lpfltclsmstlesvtylpekgl-ycgrlpssrthggteslkgknten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 2890.5;
89.9%; Pred. No. 6.3e
                                                          Human hippocampal sel-10 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 43-46; 91pp; English.
                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                         Pauley AM;
                                                                                                                                                                                                                                        98WO-US26820.
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                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                      Li J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 551; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 AA;
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                                                                                                                                          Homo sapiens
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DB 22; Length 627;

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isolated human sel-10 polypeptides

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           ANGOGOORRRITSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEP
                                                                                                                                                                                 NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE
    ------RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRA
                                                    OFORDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPL
                                                                                                   VSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECI
                                                                                                                           HTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRV
                                                                                                                                                   VSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCI
                                                                                                                                                                           HTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK
                                                                            HIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRI
                                                                                                                                                                                                                                                                                                                  Alzheimer's disease; PS-1; PS-2;
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therapy; mammary gland.
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                           This sequence is an epitope-tagged version of a human sel-10 protein of the invention. The human sel-10 proteins of the invention are isolated from hippocampus and mammary gland. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease.
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                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                          Length 666;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                            DB 20;
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89.9%; Pred. No. 7e-274;
iive 11; Mismatches 10;
                                                                                                                                                                                                                                                                        13 LVPVDLKSAKEPLPHQTVMKIFSISIIA----QGLPFCRR---
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Example 3; Page 85-88; 91pp; English
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                                                                                                                                                                                    New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                        The present invention relates to human sel-10. The sel-10 proteins of
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                                                                                                                                                                                                                                                                                                                                                                                      Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                            13 LVPVDLKSAKEPLPHQTVMKIFSISIIA----QGLPFCRR---
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=:
        Sel-10; human; Alzheimer's disease; Abeta
                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                   3; Page 108-112; 116pp;
                                                                                                                            (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                 Li J;
                                                                                                        99US-0328877.
                                                                                      2000WO-US09814.
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 551; Conservative
                                                                                                                                                Gurney ME,
                                                                                                                                                                  WPI; 2001-102404/11.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         666 AA;
                                               WO200075328-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 -----
                            Homo sapiens.
                                                                                     23-MAY-2000;
                                                                                                        09-JUN-1999;
                                                                 14-DEC-2000
                                                                                                                                              Pauley AM,
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                      Example
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This sequence is an epitope-tagged version of a human sel-10 protein of the invention. The human sel-10 proteins of the invention are isolated from hippocampus and mammary gland. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (FS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sel-10; human; presentlin; Alzheimer's disease; PS-1; PS-2; hippocampus;
therapy; mammary gland.
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                                                                                                                           HTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK
                         517 NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE
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Pred. No. 7e-274;
1; Mismatches 10;
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                                                                                                                               NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE
                                                                                                                                                                                                                      QFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPL
                                                           HIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRI
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r raising antibodies
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the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting selling polypeptide expression. The sello polypeptides are also useful as drutargets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abete. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
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89.9%; Pred. No. 7e-274;
ive 11; Mismatches 1
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                                                                                                                                                                                                                                                        Length 592;
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Pred. No. 6.5e-
3; Mismatches
                                                                                                                                      New isolated human sel-10 polypeptides
                                                                                                                                                     Claim 24; Page 47-50; 91pp; English
                                                                                  (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                 Li J, Pauley AM;
                                                                  97US-0068243.
                                                                                                                                                                                                                                                        92.0%;
93.4%;
                                                    98WO-US26820.
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.4
Matches 549; Conservative
                                                                                                              WPI; 1999-458026/38.
                                                                                                                                                                                                                   Alzheimer's disease
                                                                                                                                                                                                                                 592 AA;
                                                                                                                        N-PSDB; AAX99701
                      WO9932623-A1
                                                                  19-DEC-1997;
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The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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Pred. No. 6.
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                                                                                                                                                                                                                                                               Human hippocampal sel-10-2 protein
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Score 2889; DB 20; Pred. No. 7.1e-274; 1; Mismatches 0;

91.9%; 99.8%;

Conservative

Best Local Similarity Matches 540; Conserv

Query Match

Length 545;

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their encoding polynucleotides, detecting sel-10 polypeptide the treatment of Alzheimer's disease
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RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRIT
          SVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPK
                                                    ELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGF
                                                                                            IHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVW
                                                                                                                                     KLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDM
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Claim 1; Page 72-75; 116pp; English.

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The present invention relates to human sel-10. The sel-10 proteins of antibodies useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's alsease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
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                                                                                                                                                                                                                     Length 545;
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                                                                                                                                                                                                                  91.9%; Score 2889; DB 22;
99.8%; Pred. No. 7.1e-274;
iive 1; Mismatches 0;
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Best Local Similarity 99.8
Matches 540; Conservative
                                                                                                                                                                             545 AA;
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Search completed: September 25, 2001, 14:41:10 Job time: 165 sec

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55 DHGSEVRSFSLGKKPC----KVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSV 110
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 02/06/899,578
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 05/5/53200/JPW/AKC
FELEFHONE: (212) 278-0400
TELEFRANCE/DOCKET NUMBER: 05/5/53200/JPW/AKC
TELECOMMUICATION INFORMATION:
TELEFONE: (212) 278-0400
TELEFRAN: (212) 278-0455
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 587 amino acids
mwnb: amino acids
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45.6%; Pred. No. 2:1e-116;
tive 85; Mismatches 162;
               US-07-626-589-2
US-08-190-802A-57
US-08-130-444A-1
US-08-236-410-2
US-08-465-421-2
US-08-965-600-1
US-08-965-600-1
US-08-965-600-1
US-08-965-600-1
US-08-965-600-1
US-08-965-600-1
US-08-965-600-1
US-08-190-802A-39
US-09-060-886-3
US-09-184-445-3
US-08-190-802A-45
US-08-190-802A-45
US-08-190-802A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                                                                                                                        September 25, 2001, 14:39:00; Search time 13.65 Seconds
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Sequence 32,
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Sequence 3,
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/cgn2_6/ptodata/2/iaaAcBe_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-08-190-802A-30
US-08-283-917-3
US-08-961-716-3
US-08-961-716-9
US-08-961-716-9
US-08-190-802A-51
US-08-190-802A-52
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S-08-190-802A-66
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S-08-646-715-5
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S-08-190-802A-63
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- 08 - 646 - 715 - 18

- 09 - 063 - 743 - 1

- 08 - 190 - 802A - 64

- 08 - 190 - 802A - 68

- 08 - 308 - 818 - 2
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US-08-190-802A-31
US-08-190-802A-38
US-09-180-783-2
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                                                                                                                                                                                                                                                                                                                              197339 seqs, 20590346 residues
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                 GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                         --GIDEPLHI-----KRRKVIKPG--FIHSPWKSAYIRQHRIDTNWRRGELKSPKVL
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
CLASSIELATION: 435
ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
CORRESPONDENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/53200/JPW/AKC
REEECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                  171 ALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFD 585
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                                                                                                                         211
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                                                                                                                                                                                                                                                                                                                              378 VLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIH-- 435
                                                                                                                                                                                                                                                                                                                                                 436 VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQC 495
                                                                                                                                                                                                                                                  SGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                              50 SGSTDRTVKVWS-----GHTSTVRCMAMAGSILVTGSRDTTLRVWD-----
                                                                                                                                   74;
                                                                                             Length 209;
                                                                                                                                   35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                               Score 671; DB 3;
Pred. No. 8.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496 LQTLQGPNKHQSAVTCLQ-FNKNFVITSSDDGTVKLWD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 -----GHRSAITSLQWFGRNMVATSSDDGTVKLWD 209
                                                                               21.3%; Scur No. 5.... 52.2%; Pred. No. 5.... 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8600-0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/08190802A; Patent No. 5519003; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 517 amino acids
amino acid
                                                                                                                                     Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-899-578-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                  Similarity
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                                                                                               Query Match
Best Local Simi
Matches 145;
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NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIYAK, MCCLELLAND, MAIER
ADDRESSEE: NEUSTADT, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714 -DQIWSVNFKGKTLVAAV-EKDG--QSFLEILDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08283917
Patent No. 5849557
 REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                     779 amino acids
                                                                                                                                                     protein
                                                                                                                         MOLECULE TYPE: proteil
HYPOTHETICAL: NO
ANTI-CPMCT
                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: US-08-190-802A-32
                                                                                                                    amino acid
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                                                                                  13;
                                                                                                               60 VRSFSLGKKPCKVSEYTSTTGLVPCSATPT---TFGDLRAANGQGQQ---RRRITSVQPP 113
                                                                                                                                                                               114 TGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLP----KE 169
                                                                                                                                                                                                 170 LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKE-----EGIDEPLHIKRR 221
                                                                                                                                                                                                                                                                             121 IAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAE----RR 175
                                                                                                                                                                                                                                                                                                             K-----VIKPGFIHSPWKSAY-----IRQ--HRIDINWRRGELKSPKV-LKGHDDHVI 266
                                                                                                                                                                                                                                                                                                                                       176 GWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGV 235
                                                                                                                                                                                                                                                                                                                                                                                TCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMGHV 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIRVMDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG------Q 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEGFSCSLQPPTASEREDCNRDEPPRKIITEKNTLRQTKLANGTSSMIVPKQRKLSANYE 60
                                                                                                                                                                                                                                                                                                                                                                                                  AAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDT
                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses:
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                 Length 517;
                                         19.8%; Score v...;
31.1%; Pred. No. 2.6e-54;
+ive 89; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|| :| | |||: :|| | || 475 CLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILLIWD 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 CLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD 532
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Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R.
                                                               Best Local Similarity 31.1%
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-190-802A-32
US-08-190-802A-30
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                               267
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247 LFRLVANMDRSELSDLGTLIKDNLKRDLITSLPFEISLKIFNYLQFEDIINSLGVSQNWN 306
                                                                                                                                                                                                                                                                                                                                                           194 RILAEDNLLWREKCKEEGIDEP----LHIKRRKVIKPGFIHSPWKSAYIRQHRIDINWR 248
                                                                                                                                                                                                                                                                                                                                                                                                366 ----YNPKFVPQRTTLRGHMTSVITCLQFEDNYVITGADDKMIRVYDSINKKFLLQLSGH 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 RVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIH----VVSGSLDTSIRVWDV 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 -ANDYSRKFSYHHTNLSAITTFYVSDNILVSGSEN-QFNIYNLRSGKLYHANILKDA--- 713
                                                                                                                                                                                                                                         135 LDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYW- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 TGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRGHMASVRTVSGHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGELKSPK - - - - - VLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TGGVWS-SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHE----KRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 KTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 ENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSAAADGSIRGWD-
                                                                                                                                                                               81;
                                                                                                                       Length 779;
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GENERAL INFORMATION:
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: ARAI, HIROYUKI
APPLICANT: ARAI, HIROYUKI
TITLE OF INVENTION: AND GENE THEREOF
TITLE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                  Indels
CDC4 / CDC20 protein, Fig. 15
                                                                                                                 Query Match 19.7%; Score 618.5; DB 1;
Best Local Similarity 29.6%; Pred. No. 1.5e-53;
Matches 152; Conservative 105; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKMMDVSTGMCLMTLVGHDNWVRGVLFHS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPYTRVIFHPVESVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 --NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VLKGHD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 439; DB 2; Length 409; 30.1%; Pred. No. 7.2e-36; tive 62; Mismatches 133; Indels
: 1755 S. Jefferson Davis Highway, Suite 400 Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 GFIHSPWKSAYIRQHRI-------DTNWRRGELKSPK--
                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURFENT APPLICATION DATA:
                                                                                                                                                                                                APPLICATION NUMBER: US/08/283,917
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: JP 20943/1993
ATTORNEY, AGENT INFORMATION:
NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-030-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
_US-08-961-716-3
; Sequence 3, Application US/08961716
                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEK: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.1:
Matches 110; Conservative
                                STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unk
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VWECR 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM:
US-08-283-917-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 GLLEKKWISVIRLOKKVMELESKLNEAKEEFISGGPLGQKRDPKEWIPRPPEKYALSGHR 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 439; DB 2; Length 409; 30.1%; Pred. No. 7.2e-36; Live 62; Mismatches 133; Indels
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INOUE, KEIZO
APPLICANT: AROU, HIROYUKI
APPLICANT: ARIO, KIZO
APPLICANT: ARIO, KIZO
APPLICANT: ARIO, KIZO
APPLICANT: ARIO ENZYME
TITLE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-A0G-1994
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-A0G-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-030-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 GFIHSPWKSAYIRQHRI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELES: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 amino acids
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Best Local Similarity 30.19
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Bos taurus
US-08-961-716-3
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STRANDEDNESS: unl
                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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229 TFTGHREWVRMVRPQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISMAPES 288
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         432 -------DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473
                                                                                                                                                                                                                                                                                    349 GGKFILSCADDKTLRVWDYKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDQTVK 405
                                                                         378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF----
                                                                                                                                                                                                                                                          474 --NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INUG, KEIZO
APPLICANT: ONIOL, KEIZO
APPLICANT: ARAI, HIROYUKI
TITLE OF INVENTION: AND GENE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBLON, SPIVAK, MCCLELLAND, MAIER &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 439; DB 2;
Pred. No. 7.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-406-1994
FILING DATE: 03-AUG-1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Oblon, No. 5880272man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 9, Application US/08961716
; Patent No. 5880272
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEBRAY. 7777, 13-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%;
30.1%;
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 410 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  406 VWECR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                     530 LWDLK 534
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ADDRESSEE:
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288 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKMMDVSTGMCLMTLVGHDNWVRGVLFHS 347
                                                                       348 GGKFILSCADDKTLRVWDYKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDQTVK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DINWRRGELKSPK------VLKGHD 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
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                                          474 -- NILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INOUE, KEIZO
APPLICANT: INOUE, KEIZO
APPLICANT: ARAL, HIROYUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 439; DB 2; Length 41 30.1%; Pred. No. 7.2e-36; ive 62; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,917
FILING DATE: 03-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Oblon, NO. 5849557man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-030-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DABER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08283917
Patent No. 5849557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 GFIHSPWKSAYIRQHRI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                405 VWECR 409
                                                                                                                                     530 LWDLK 534
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; INDIVIDUAL ISOLATE: LIS1 (human), F1g.
US-08-190-802A-51
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STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                       13.5%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 212 amino acids TYPE: amino acid
                                                                                                     Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: U.S.A.
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 LWDLK 534
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                                                                                                   DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                           289 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHS 348
                                                                                                                                                                                                                                                                                                                                                                                                       349 GGREILSCADDKILRVWDYKNKRCMKIL---NAHEHFVISLDFHKTAPYVVTGSVDQTVK 405
                                 227 GFIHSPWKSAYIRQHRI------DTNWRRGELKSPK------VLKGHD 262
                                                              49 GLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPKEWIPRPPEKYALSGHR 108
                                                                                                                                     109 SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 168
                                                                                                                                                                      320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                                                                         378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               474 --NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK
   90;
 Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: When Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSEE: P.O. Bohlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PACENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: O1-FEB.1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51, Application US/08190802A Patent No. 5519003
 62;
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TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 409 amino acids TYPE: amino acid
Matches 110; Conservative
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ORIGINAL SOURCE:
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406 VWECR 410
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COUNTRY:
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                                                                                                                                                                                                                                 474 --NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK 529
                                              Indels 61; Gaps
                                                                                                                                                   49 GLLEKKWISVIRLQKKVMELESKLNEAKEEFTSGGPLGQKRDPKEWIPRPPEKYALSGHR 108
                                                                                                                                                                                                                                                                                                     320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                                                                                                                                                                                                                                     378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 GGKFILSCADDKTLRVWDYKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDGTVK 404
     Length 409;
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                                                                                               227 GFIHSPWKSAYIRQHRI------DTNWRRGELKSPK
Score 424.5; DB 1;
Pred. No. 2.1e-34;
62; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
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117 QEWLK----MFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELAL 172
                                                                                                                                                                                                                                                                                     243 SGSADFAVKVWALSAGTCLNTLTGHTEWV------TKVVLQKCKVKSLLH 286
                                                                                                                                                                                                                                                                                                                                              222 KVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                 282 DNTLKVWSAVTGKCLRT--LVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 YGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRR--VV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIH 457
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                                                                                                                                                                                                                                                           173 YVLSFLEPKDLLQAAQTC-----RYWRILAEDNLLWREKCK-----EEGIDEPLHIKRR 221
                                                                                                                                                                                                    458 TLTGHQSLTSGMELKDNILVSGNADS-TVKIWDIK---TGQCLQTLQGPNKHQSAVTCLQ
                                                                                       12.0%; Score 376.5; DB 1; Length 422; 25.6%; Pred. No. 1.6e-29; Live 75; Mismatches 140; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-190-802A-66
; Sequence 66, Application US/08190802A
; Patent No. 5519003
; Patent No. 519003
; PALICANT: Mochly Rosen, Daria
APPLICANT: Ron, Dorit
; TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; UNMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. BOX 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/190,802A FILING DATE: 01-FEB-1994 CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 ----FNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLE 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
    ; INDIVIDUAL ISOLATE: MD6, Fig. 35
US-08-190-802A-52
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ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                           Best Local Similarity 25.68 Matches 117; Conservative
                                                                                         Query Match
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                                                                                                                                                                                                           260 GHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWS-SQMRDNIIIS 318
                                                                                                                                                                                                                                                                                            319 GSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHE----KRVVSGSRDATLRVWDIETGQ 374
                                                                                                                                                                                                                                                                                                                                                                                 375 CLHVIMGHVAAVRCVQYDGRRVVSGAXDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGI 434
                                                                                                                                                                                                                                                                                                                                                                                                         93 -----KGHMASVRTVSGHGNIVVSGSYDNTLIVWD-------GHTDRIYSTIYD- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 H----VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDI 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                       50 GSTDRTVRVWD------GHNSTVRCLDIVEYKNIKYIVTSGRDNTLHVW-----
                                                                                                                                                                        78;
                                                                                                                            Length 212
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Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses:
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREE: P-0. Box 60850
CITY: P-10 Alto
                                                                                                                                                                      60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                            13.0%; Score 410; DB 3; 34.9%; Pred. No. 2.1e-33;
                                                                                                                                              Local Similarity 34.9%; Pred. No. 2.1e-
nes 96; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 KTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDD 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 HT------NLSAITTEYVSDNILVSGSEN 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 422 amino acids
amino acid
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                        linear
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                   ; TOPOLOGY: 11.; MOLECULE TYPE: US-08-899-578-7
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Weinzierl, Robert O.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 704 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.0%
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-188-582-5
                                     San Francisco
                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                ZIP: 94111-4187
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ITV 661
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
                                                                                         COUNTRY:
     STREET:
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DRTVRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFD--HTGKKPSTPEEAQKK 355
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.6%; Score 364.5; DB 1; Length 514; Best Local Similarity 23.0%; Pred. No. 3.6e-28; Matches 119; Conservative 116; Mismatches 153; Indels 129;
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Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Ruppert, Siegfried
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                LENGTH: 514 amino acids TYPE: amino acid
                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-190-802A-66
                                                                                                                                                                                                                           ANTI-SENSE: NO
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US-08-188-582-5
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315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTV-RCMHLHEKR-VVSGSRDATLRVWDIET 372
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
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10.0%; occ. 1.2e-24;
Best Local Similarity 29.0%; Pred. No. 1.2e-24;
Matches 88; Conservative 61; Mismatches 126; Indels
                                                                     NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
CONTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILIG DATE: 09-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-190-802A-62;
Sequence 62, Application US/08190802A;
Patent No. 5519003;
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 704 amino acids
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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ITV 661
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315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTV-RCMHLHEKR-VVSGSRDATLRVWDIET 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F--DGIHVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELK--DNILVSGNADSTVK 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 VLKGHDDHVITCLQFC--GNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 WSCVVTYRGHVYPVWDVRFAPHGYYFVSCSYDKTARLWATDSNQALRVFVGHLSDVDCVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 IWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSD--DGTVKLWDLK--TGEFIRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%; Score 326; DB 1; Length 704; 28.7%; Pred. No. 4.7e-24; Indels iive 63; Mismatches 125; Indels
                APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: PO. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TIIF, F1g.
US-08-190-802A-62
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 25, 2001, 14:41:34 Job time: 154 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SED ID NO: 62:
SEQUENCE CHARACTERISTICS:
Mochly-Rosen, Daria
                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 amino acids
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Best Local Similarity 28.7%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 94306-0850
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repeat protein

	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	322	324.5 322 318.5	10.3
OM protein - pro	OM protein - protein search, using sw model	2 8 8 4 8	318 317 315.5	10.1 10.1 10.0
Run on:	September 25, 2001, 14:39:35; Search time 17.58 Seconds (without alignments)	36 37 38	314.5 314 312	10.0 10.0 9.9
Title: Perfect score: Sequence:	C33Z-131 MILLION CELL UDGALES/SEC US-09-328-877A-8 3143 13143 CELL UDGALES/SEC 1 MKKDGKDPT NHGLUDUNIKE CONCRETENTIVI DENVINA FOO	8 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	311.5 311 311 310.5	ത്യ യ യ യ
able:	E MONTONE LINEAGUA FVOLENOSANGIEEINLLVILEDVOMN 289 BLOSUM62 Gapop 10.0 , Gapext 0.5	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	310 306 304.5	200 27.7.
Searched: Total number of	Searched: 219241 seqs, 76174552 residues Total number of hits satisfying chosen parameters: 219241			

probable pleiotron WD-40 repeat regul WD repeat protein Protein TipD - sli PRL2 protein - Ara neuronal different hypothetical protein probable GTP-bindi hypothetical protein WD40 repeat regul TATA box-bindiep potein

T50289 T50289 JN0983 JN9905 T40905 T408602 JC7588 S38108 T14273 T

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

summaries

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

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Database :

seq length: 0 seq length: 2000000000

DB DB

Minimum Maximum

11;

2.3

2

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A;Molecule type: DNA
A;Residues: 1-640 <ODE>
A;Cross-references: GB:247047; EMBL:246861; NID:9603997; PID:9763300; MIPS:YIL046w
R;Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
                                                                                                                                                                                 MET30 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein Y19905.02; protein Y1L046w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
C;Accession: S49932, 843750
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: S49931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKYSNSNDKIRKLILDGILSTSCFP-QLSYISSLVTHMIKIDFISILPQELSLKILSYLD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSSPDLATNDSGTRVQPLPEYNFTK------FCYR-----HNPDIQ-FSPT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKPC-----KVSEYTSTTGLVPCSATPTTFGDLRAANGQGQRRRITSVQPPTGLQEWL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KMFQSWSGPEKLLALDELID-SCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEP------LHIKRRKVIKPGFI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSNADIQTQTTRPWKVIXRERFKVESNWRKGHCRIQE-FKGHMDGVLT-LQFNYRLLFT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || |:|: :| ||| :| || || || || || GSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLYFDDRKLITGSLDKTIRVWNYITGECIST 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 PTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRRMKRKLDHGSEVRSFSLG 66
474 -IEGVWEIAADHLRLISGAHDGVVKVWE--ACECVHTLK---NHSEPVTSVALGDCEVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS------PWKSAYIRQHRIDINWRRGELKSPKVLKGHDDHVITCLQFCGNRIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 LYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGR--RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%; Score 650; DB 2; Length 640;
26.4%; Pred. No. 2.9e-43;
Live 114; Mismatches 197; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: 9L
C.Superfamily: unassigned WD repeat proteins; WD repeat homology
F.298-329-Domain: WD repeat homology <WD1>
F.338-369/Domain: WD repeat homology <WD2>
F.314-409/Domain: WD repeat homology <WD3>
F.317-409/Domain: WD repeat homology <WD3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-60, I',62-640 <THO>
A;Cross-references: EMBL:L26505; NID:9432493; PID:9432494
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 VSGAYDFMVKVWDPETETCLHTLQGHTNRVYSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SGD:MET30
A;Cross-references: SGD:S0001308; MIPS:YILO46w
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Best Local Similarity 26.4%; Pre
Matches 163; Conservative 114;
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A; Accession: S43750
                                                                   |:|| : ||
GSEDGKIYLW
                                            522 SSDDGTVKLW
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MET30 protein -
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                                                                                                                                                                                                                                                                                                              probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe) c; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000 C; Accession: T38932 R; Badcock, K.: Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. A; Reference number: 221818 A; Reference number: 221818 A; Accession: T38932 A; Accession: T38932 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-605 cabb. A; Residues: 1-605 cabb. A; Residues: 1-605 cabb. A; Cross-references: EMBL:294864; PIDN:CAB08168.1; GSPDB:CN00066; SPDB:SPAC57A10.05c A; Experimental source: strain 972h-; cosmid c57Al0 A; Genetics: A; Map posttion: 1 C; Superfamily: unassigned WD repeat profesion was accessed.
                                                                                                                                                                                                                                                                                                                                                  (aqwod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                  TGQCLQTLQGPNKHQSAVTCLQ-FNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGS 550
                                                                                                                             424 IVCSGSLDTSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDIH 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 KRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : :|||||: : | |||| ::|: ||:|| |::
SFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQHINRKCEKCGWGLPLLERNTL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 OPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521
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29.8%; Pred. No. 1.1e-45;
:1ve 93; Mismatches 181; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 ALYVLSFLEPKOLLQAAQTCRYWRILAEDNLLWREKCKE----
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Oy 166 LPKELALYVLSFLEPKDLLCAAOTCRYW-RILAEDNLLWREKCKEEGIDEPLHIKRR 221 1 1 1 1 1 1 1 1 1 1	Qy 371ETGQCLHVLMGHVAAVRCUQYDGRRVVSGAYDFWKVWDPETE Db 478 TDPPYLPDNTNSIDRWEKNPFYPTLIGHTDSVRTISGYGDLLVSGSYDSSIRIWRVSTG Qy 414 TCLHTLQGHTNRVYSLQPDGIH-VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMEL	RESULT 5 T16607 hypothetical protein K10B2.1 - Car C;Species: Caenorhabditis elegans C;Date: 20.Sep-1999 #sequence_rev C;Accession: T16607 R;Miller, N. submitted to the EMBL Data Librar. A;Description: The sequence of C. A;Reference number: Z18545 A;Accession: T16607 A;Status: preliminary; translated A;Molecule type: DNA A;Status: preliminary; translated A;Molecule type: DNA A;Status: references: EMBL:U28730; I A;Experimental source: strain Brii C;Genetics: A;Gene: CESP:K10B2.1 A;Introns: 78/3; 125/1; 183/2; 28; Query Match	Best Local Similarity 33.5%; Pred. No. 2.2e-42; Matches 154; Conservative 80; Mismatches 167; Indels 59; Gaps 12; Qy 126 WSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFORDFISLLPKELALYULSFLEPKDLLQ 185
Db 437 FSCSDDTTIRMWDIRTNSCLKVFRGHVGQVQKIIPLTIKDVENLATDNTSDGSSPQDDPT 496 Qy 430 QFDG	MESULT 4 743557 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe) N.Alternate names: proteolysis factor sudlp C.Species: Schizosaccharomyces pombe C.Species: Schizosaccharomyces pombe C.Species: Schizosaccharomyces pombe C.Saccession: T43557, T38794, T43798 R.Wolf, D.A.; Jackson, P.K. submitted to the EMBL Data Library, December 1997 A.Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in A.Reference number: 222576 A.Steus: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-703 <wol> A.Residues: 1-703 <wol> A.Residues: 1-703 <wol> A.Residues: strain h- 972</wol></wol></wol>	M.A.; Wood, V. 00066; SPDB:SPAC4D7.03 ted Cdc18 and Rum1 proteins 9496.1; PID:g3293383	Query Match 20.4%; Score 641; DB 2; Length 703; Best Local Similarity 27.3%; Pred: No. 1.7e-42; 1.7e-42; Matches 178; Conservative 111; Mismatches 248; Indels 116; Gaps 17; 1 Qy 9 LNHGLVPVDLKSAKEPL

plo

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A;Residues: 1-775 <WOO>
A;Cross-references: EMBL:AL022103; PIDN:CAA17898.1; GSPDB:GN00067; SPDB:SPBC2G2.18
A;Experimental source: strain 972h-; cosmid c2G2
                                                                                                                                                                                                                    C; Species: Schizosaccharomyces pombe
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C; Accession: T45136; T40157
Submitted to the EMBL Data Library, September 1996
A; Description: Fission yeast WD repeat protein Popl is involved in maintenance of A; Accession: T45136
A; Atcession: T45136
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T45136
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                  repeat protein pop1 (imported) - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 SVQPPTGLQEW----LKMFQSWSGPEKL-----LALDELIDSCEPTQVKHMMQVIEPQF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDVWTFEYVGD 457
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416 TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTL 475
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TLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTTDTDDVEKENRPASND 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 AGTDAKIRIWNLESGELLQTLHGHSNLVSQVTFNQNILVSASAPPDTSLRVWDLNTGSCR 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.; Churcher, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain h- 972
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, submitted to the EMBL Data Library, March 1998
A; Reference number: 221842
A; Accession: T40157
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                         495 CLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD 532
                                                                    A;Residues: 1-775 <KOM>
A;Cross-references: EMBL:Y08391; PIDN:CAA69671.1
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Matches 153; Conserv
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A: Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
B4808

B48088

beta-transducin repeat-containing protein - African clawed frog
N;Alternate names: beta-Trcp
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C;Accession: B48088
R;Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Call. B40.1 13, 4953-4966, 1993
A;Title: Saccharomyces corevisiae cdc15 mutants arrested at a late stage in anaphase are A;Reference number: A48088; MUID:93330289
A;Title: Saccharomyces corevisiae cdc15 mutants arrested at a late stage in anaphase are A;Reference number: A48088; MUID:93330289
A;Status: prelliminary
A;Molecule type: mRNA
A;Residues: 1-518 45PE>
A;Cross-references: GB:M98268; NID:9295542; PIDN:AAA02810.1; PID:9295543
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
C;Keywords: duplication
F;431-462/Domain: WD repeat homology <WDI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                320 VRVWDVETGECIKTLIHHCEAVLHLRFANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVG 379
                                                                                                           441
                                                                                                                                                                                                                         : :| |: || :: :: :: || KEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLKPMLQRDFITALPARGLDH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 VRSFSLGKKPCKVSEYTSTTGLVPCSATPT---TFGDLRAANGQGQQ---RRRITSVQPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLQEWLXMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLP----KE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-----VIKPGFIHSPWKSAY----IRQ--HRIDINWRRGELKSPKV-LKGHDDHVI 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASATDITLRRVLVGHR 355
                  LKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG-----Q 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 HVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKE------EGIDEPLHIKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                      -- CLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD 532
                                                                                                                                                                                                                                                                                                                  500 EICLCSLV---QHTGRVFRLQFDDFQIVSSSHDDTILIWD 536
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Best Local Similarity 31.19
Matches 161; Conservative
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Db 366YNPKEVPQRTTLRGHMTSVITCLQFEDNYVITGADDKMIRVYDSINKKFLLQLSGH 421 Qy 303 TGGVWS-SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVV 357	QY 395 RVVSGAVDEMVKWDPETETCLHTLQGHTRRVYSLQFDGIHVVSGSLDTSIRVWDV 1	RESULT 9 T18521 T18521 T18521 Det at ransducin-like protein - Podospora anserina C; Species: A; Turcq, B.; Bequeret, J. Gane 162, 135-139, 1995 A; Title: A gene responsible for vegetative incompatibility in the fungus Podospora A; Reference number: 21844; MUID:96009891 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Cross-references: EMBL:L28125; NID:9607002; PID:9607003; PIDN:AAA85775.1 C; Genetics: A; Gene: het-el A; Introns: 761/3	Query Match 18.5%; Score 582.5; DB 2; Length 1356; Best Local Similarity 28.9%; Pred. No. 1.8e-37; Matches 169; Conservative 85; Mismatches 193; Indels 137; Ga QY 113 PTGLOEWLKM	Db 710 SSTSSKWVHLLQDDGDIHRFLTTKYLYWLEALSLLRALPEGINAIRQLESLLGHTIRGRL 769 Qy 223VIKPGFIHSPWKSAYIRQHRIDTN 246
OY 497 QTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWR 556	RESULT 8 S56245 cell division control protein CDC4 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YEV009w C;Species: Saccharomyces cerevisiae C;Date: 02-Sep-1995 #sequence_revision 12-Apr-1996 #text_change 26-May-2000 C;Accession: S56245; S48310; A26867; S62304 R;Murakami, Y.; Maitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu submitted to the EMBL Data Library, May 1995 A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce A;Reference number: S56186 A;Mccession: S56245 A;Molecule type: DNA A;Residues: 1-779 <mur></mur>	Σ ο	0; NID:g836814; PIDN:BAA06495.1; PID:d1007066; 85; MIPS:YFL009w NA replication; separation of the spindle poleepeat proteins; WD repeat homology mology <wd1> mology <wd2> %; Score 618.5; DB 2; Length 779; %; Fred.No. 1.2e-40; 7.3e.</wd2></wd1>	MACCHES 132; CONSELVATIVE 105; MISMATCHES 176; Indels 81; Gaps 16;

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	Db 426 RTVFSASDDTTIKLWDLDTRQVIRTYEGHVGHVQQVLILPPEYEPDEEVLNGASQDNQDA 485	Qy 432 435 Qy 432 435 Dy 432 435	436VVSGSLDTSIRVWDVETGNCIHTLTGHOSLTSGMELKDNI-LVSGNADSTV	240 DEPTREMIGGLDSIMRUMDSALGNCER LEGGREGGNEGGGTT - DILRYISGANDGN 486 KIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDBGTVKLWDLK 534	Db 601 KTWEPRSGKCDATYTGHCGPVTCVGLSDSLMASGSEDGTIRLHSFK 646 RESULT 11	T50211 WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; bate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000	C; Accession: T50211 R; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, submitted to the EMBL Data Library, January 2000 A; Reference number: 225046	ro	A; Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05 A; Experimental source: strain 972h(-); cosmid c30	C)GENELICS SPACE (1); SPDB:SPACE (0); A;Map position: 1 A;Introns: 43/1; 74/3	C;Superfamily: unassigned WD repeat proteins; WD repeat homology	Query Match 17.0%; Score 533; DB 2; Length 506; Best Local Similarity 25.8%; Pred. No. 3.5e-34; The Matches 140; Conservative 91; Mismatches 204; Indels 108; Gaps 14;	Qy 55 DHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGOORRRITS 109 1	110 VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHWMQVIEPQFQRDFISILPKE	DD 45 IRDLLASLSKEGVVAVYNHVRSLLFTDFTEVFPEE 79	UNITY DOF DEFENDED TO THE TOTAL THE STATE OF	OY 217HIRRRKVIKP-GFIHSPWKSAYIRQHRIDTNWRRGE- 251	252LKSPKVLKGHDDHVITCLOFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVG	Db 200 LVSTENNPSIREPADQDERATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYG 259 Qy 302 HTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSG 359	Db 260 HSGSVLCLDFCRRNLLVSGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISS 319 Ov 360 SRDATLRVWDIETGOCLHVLMGHVAAVRCVOYDGRRVVSGAYDFWVKVWDPETE 413	320 SRDHTARVWRLDATSPAEACMHVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTG	QY 414 TCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473
Db 886 VWSVAFSPDRER-VASGSDDKTIKIWDAASGTCTQTLEGHGGRVQSVAFSPDGQRVASGS 944	Qy 361 RDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHT 418	::: :	QY 419 LOCHTNRYVSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHOSLTSGWELK 472 :	QY 473 DNILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL 530 1063 GQRVASGSDDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQRVASGSIDGTIKI 1119	QY 531 WDLKTGEPIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGT 574	RESULT 10 T46660	<pre>sulfur controller-2 protein [imported] - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Bate: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000 C;Accession: T46660</pre>	R;Kumar, A.; Paietta, J.V. Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995 A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes A:Reference number: 223121: WID:95241499	A;Accession: T4660 A;Stetus: preliminary; translated from GB/EMBL/DDBJ	A;Wolecule 'type: DWA A;Residues: 1-650 <kum> A;Cross references: EMBL:U17251; NID:g806757; PIDN:AAA68968.1; PID:g806758 C;Genetics:</kum>	A;Gene: scon-2 A;Map postLon: 3 A:Tntrone: 75/3: 319/1: 354/1	A: Description: (979; 919/1; 954/1 C:Function: A:Description: negatively regulates sulfur structural gene expression A:Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to	Olioty Match	Similarity 26.3%; Pred. No. 1.9e-37; Indels 5; Conservative 84; Mismatches 177; Indels	Qy 106 RITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDS-CEPTQVKHMMQVIEPQFQRDFIS 164 :-	165 LLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPL	TVSLTKAAQVSQRWRTLADSDA	189 LERKKLRNYTRQRQLAKGGPQGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQC	QY 228FIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNR 275 1 17 18 18 18 18	Qy 276 IVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGEC 335 :: : : : :	336 IHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGCCLHVLMGHVAAVRCVQYDG	Db 367 LSTFAAHTDSVISVHFDGHLLASGSSDKTVKIFDFNSKE-TYCLKGHSDWVNSTHVDIKS 425 Qy 394 RRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF

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A; Molecule type: mRNA
A; Cross-references: EMBL:D30615
A; Title: Miller-Tobleker lissencephaly gene encodes a subunit of brain platelet-activat
A; Title: Miller-Tobleker lissencephaly gene encodes a subunit of brain platelet-activat
A; Title: Miller-Tobleker lissencephaly gene encodes a subunit of brain platelet-activat
A; Reference number: S48075
A; Contents: annotation
A; Molecule type: mrNa
A; Reference number: S51606
A; Molecule type: mRNA
A; Reference number: S51606
A; Molecule type: mRNA
A; Residues: 1-25, A', Z7-153, E', 155-410 < HAM>
A; Cross-references: EMBL:D30615; NID:9516665; PIDN:BAA06305.1; PID:d1006869; PID:9551
C; Superfamily: unassigned WD repeat proteins; WD repeat homology < WD3>
F; 186-179/Domain: WD repeat homology < WD3>
F; 188-221/Domain: WD repeat homology < WD5>
F; 289-263/Domain: WD repeat homology < WD5>
F; 334-367/Domain: WD repeat homology < WD5>
F; 376-409/Domain: WD repeat homology < WD5>
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A;Title: Isolation of a Miller-Dieker lissencephaly gene containing G protein beta-su A;Reference number: S36113; MUID:93361119
A;Stetus: prellminary
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C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
C;Accession: S36113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPKEWIPRPPEKYALSGHR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
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30.1%; Pred. No. 6.9e-27;
Live 62; Mismatches 133;
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Matches 110; Conservative
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R; Futey, L.M.; Medley, O.G.; Cote, G.P.; Egelhoff, T.T.
Biol. Chem. 270, 523-529, 1995
A; Title: Structural analysis of myosin heavy chain kinase A from Dictyostelium. Evidence the beta-subunit of heterotrimeric G proteins.
A; Reference number: A55532; MUID:95122486
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multimer; phosphoprotein; phosphotransfera
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A/Straus: preliminary
A/Accession: A5532
A/Straus: preliminary
A/Molecule type: mRNA
A/Residues: 1-1146 < FUTY>
A/Cross-references: GB:U16856; NID:g608519; PIDN:AAA66070.1; PID:g608520
C/Genetics:
A/Introns: #status absent
C/Superfamily: unassigned WD repeat proteins; WD repeat homology
C/Reywords: autophosphorylation; coiled coil; multimer; phosphoprotein; phosp
C/Superfamily: WD repeat homology < WD2>
F/991-1022/Domain: WD repeat homology < WD3>
F/1031-1062/Domain: WD repeat homology < WD3>
F/1031-102/Domain: WD repeat homology < WD5>
F/1031-102/Domain: WD repeat homology < WD5>
F/1031-1102/Domain: WD repeat homology < WD5>
F/1031-1102/Domain: WD repeat homology < WD5>
F/1112-1143/Domain: WD repeat homology < WD5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Dictyostelium discoideum
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000
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474 NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDL
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Best Local Similarity 33.8'
Matches 97; Conservative
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T46032
WD-40 transport regulatory protein tupl homolog - Arabidopsis thaliana
N;Alternate names: protein T16K5.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 26-May-2000
C;Accession: T46032
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
A;Reference number: 223015
A;Accession: T46032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 CRIE>
A;Cross-references: EMBL:AL132965
A;Experimental source: cultivar Columbia; BAC clone T16K5
C;Genetics:
A;Map position: 3
A;Introns: 222/3
A;Note: T16K5.10
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
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                                                                                                                                                                                                                                                                              Length 409;
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H. WD repeat homology <WD2>
H. WD repeat homology <WD3>
H. WD repeat homology <WD4>
H. WD repeat homology <WD5>
H. WD repeat homology <WD5>
H. WD repeat homology <WD5>
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A; Molecule type: mRNA
A; Residues: 1-409 <RAS>
C; Genetics:
A; Gene: LIS-1
C; Superfamily: unassigned WD
F; 103-136/Domain: WD repeat
F; 145-178/Domain: WD repeat
F; 187-220/Domain: WD repeat
F; 333-366/Domain: WD repeat
F; 333-366/Domain: WD repeat
F; 375-408/Domain: WD repeat
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Best Local Similarity
Matches 99; Conserve
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363 ATLRVWDIETGQCLHVLMGHVAAVRCVQY--DGRRVVSGAYDFMVKVWDPETETCLHTLQ 420
                             421 GHTNRVYS-LQF--DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQ------SLTS 467
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VRIWTOK 315
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159 F. 274 WI 274 WI 316 WI 356 WI 438 WI 438 WI 64275 MV 64275 MV
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SEL-10 OR F55B12.3.
Caenorhabditis elegans.
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homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         emericella
                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                   1 MSKPGKPTLNHGLVPVDLKS.....SRNGTEETKLLVLDFDVDMK 589
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O13615
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Q9ukt8
P49695
Q60584
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                    93435 segs, 34255486 residues
                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                            CC4_YEAST
HET1_PODAN
SCO2_NEUCR
KMHB_DICDI
                                                                                                                                                                                                                                                                          CC4_CANAL
POF1_SCHPO
MT30_YEAST
                                                                                                                                                                                                                                                                                                                                                                                    KMHA_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                 LIS1_MOUSE
LIS1_BOVIN
YAF1_SCHPO
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Maximum Match 100%
Listing first 45 summaries
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FW1B_HUMAN
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                              OM protein - protein search, using sw model
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                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                       US-09-328-877A-8
                                                                                                                                                                                                                                                       DB
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460
446.5
439
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                                                                                                Scoring table:
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                                                                                                                    Searched:
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34 332 10.6 704 1 T2D4_DROWE P49846 drosophila 35 330 10.5 486 1 PRLI_ARATH 042384 arabidopsis 36 30 10.5 577 1 TBIL_HUMAN 060907 homo sapien 37 326 10.4 2295 1 WPB9_HUMAN 059nsi6 homo sapien 38 323.5 10.3 332 1 GBLP_DICDI PL6649 saccharomyc 41 317.5 10.1 451 1 PRLI_YEAST 012417 saccharomyc 41 317.5 10.0 612 1 T2D4_HUMAN 015542 homo sapien 015542 homo sapien 015542 homo sapien 015542 homo sapien 01542 10.0 612 1 TIPD_DICDI 015542 homo sapien 0155
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ALIGNMENTS

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RESULCAREL

10.2022-0.00 (Rel. 37) Lats sequence update)

11.002-1998 (Rel. 36, Craeated)

12.002-1998 (Rel. 37) Lats sequence update)

12.002-1998 (Rel. 37) Lats sequence update)

13.002-1998 (Rel. 37) Lats sequence update)

14.002-1998 (Rel. 37) Lats sequence update)

15.002-1998 (Rel. 37) Lats sequence update)

16.002-1998 (Rel. 37) Lats sequence update)

18.001-002-1998 (Re
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11;
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                                                                                                                                                                                                                                                                                                                                                                                        HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIH- 435
                                                                                                                                                                                                                                                                                                                                                                                                                    423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                     DHGSEVRSFSLGKKPC----KVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                               -VVSGSLDTSIRVWDV---ETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIK 491
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THE STATES,

THE STATES,

THE STATES AND THE EMBL/GenBank/DDBJ databases.

THE PROTEIN IS ESSENTIAL FOR INITIATION OF DNA

REPLICATION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA

REPLICATION AND SEPRATION OF THE SINDLE BOLIES TO FORM OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD

DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND

VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTAI-HTBI LOCUS

TRANSCRIPTION ACTIVATION (BY SIMILARITY).

SIMILARITY: CONTAINS 1 F-BOX DOMAIN.

SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                 23 DNGEE-SSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPR--------
                                                                                                           OPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKEL
                                                                                                                              ALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEE----------
                                                                                                                                                                                                                       --GIDEPLHI------KRRKVIKPG--FIHSPWKSAYIRQHRIDTNWRRGELKSPKVL
                                                                                                                                                                                                                                                                            KGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRD--NII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                             :99
39.4%; Score 1238; DB 1; Length 579; 45.6%; Pred. No. 9.4e-90; Live 85; Mismatches 162; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
01-ocr-2000 (Rel. 40, Last annotation update)
CELL DIVISION CONTROL PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic
                            Conservative
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              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Shieh J.C., Wh
Submitted (APR
                          262;
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P53699;
 Query Match
                Local
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                            Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 QGKANLDSIENVMSNEPTTQSELVDLVTKLSGFLSEANQNHLVFKLLQKTTRPT-LSTFN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYW------RILAEDN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LITDDAVIKYELQYPDQLLREWSTLPEINSAQVLYKKRKIIV-----NRWMDPKFKPHRI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DINWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S------VSGHGNKVVTCLQHDDEKVVTGVDDKCISIYSTQTGQLMKVLEGHE 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VSGSRDATLRVWD-----IETGQ-----CLHVLMGHVAAVRC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDIVFPEYPLLITGSRDHNIHVWKLPVVDDSQDYIETFEGEFDNPYLIAVLSGHTQSVRS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQYDGRRVVSGAYDFMVKVWD-PETETCLHTLQGHTNRVYS--LQFDGIHVVSGSLDTSI 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKH 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQRRRITSVQ-----PPTGLQEWLKMFQSWSG-----PEKLLALDELIDSCEPTQVKHMM 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLWREKCKEEGIDEPLHI--------KRRKVIKPGFIHSPWKSAYIRQHRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRV----
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GAAITCFEHDGLRVVSGSEK-MLKLWNVEKGTFARDLLSDVTGG----IWQVRFDYKRCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 684;
                                                                                                                                                                                                                                                                         WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                         3DD65DB31293B107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.1%; Score 725.5; DB 1; Best Local Similarity 30.8%; Pred. No. 2.2e-49; Matches 173; Conservative 102; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                  PRINTS; FRANCES, PROSITE; PSSOIB1; FBOX; 1; PROSITE; PSSO078; WD_REPEATS_1; 4. PROSITE; PSSO082; WD_REPEATS_2; 4. PROSITE; PSSO194; WD_REPEATS_REGION; Cell division; Mitosis; Sporulation; 258
                                                                                                                                                                                                                                                                                                    MD 1.
MD 2.
MD 3.
MD 5.
MD 6.
                                                                                                                                                                                            PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                                                                                            76090 MW;
                                                                                                                     EMBL; X96763; CAA65538.1; -. InterPro; IPR001680; -.
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Pfam; PF00400; WD40; 7.
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118 SFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQHINRKCEKCGWGLPLLERNTL 177
                                                                                                                                                                                                                                                                                                                                                           GENES EXPRESSION.
--- SUBONIT: SEEMS TO INTERACT WITH MET4.
--- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
--- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
--- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 SLTSGMEL-KDNI-LVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVIT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 -IEGVWEIAADHLRLISGAHDGVVKVWE--ACECVHTLK---NHSEPVTSVALGDCEVVS 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Barrell B.G., Badcock K., Copsey T., Dear S., Devlin K., Fraser A.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              -GFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTL
                                                                                                                                                                                                                                                                                                                                                                                                                    404 MVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQ
                                                                                                          178 YAAKASIQKRYERLTKRGVDQAHESSPVKKAKLDDYPTSSNEETISSVKPPSPNSDSKFF
                                                                                                                                                                                                                                            286 KVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTST
                                                                                                                                                                                                                                                                                                                                346 VRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQY - - DGRRVVSGAYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96069360; PubMed-8524217;
Thomas D., Kuras L., Barbey R., Cherest H., Blaiseau P.L.,
Surdin-Kerjan Y.;
"Met30p, a yeast transcriptional inhibitor that responds to S-
adenosylmethionine, is an essential protein with WD40 repeats.";
Mol. Cell. Biol. 15:6526-6534(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640 AA.
                                                                 --EGID---EPLHIKRKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 SSDDGTVKLW 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|| : ||
528 GSEDGKIYLW 537
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MET30 PROTEIN
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P39014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 KRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 -----W-AAFSEASCSERKLALQGILNNCSSSLLSFASSTLDSLVRLDFLSLLPVEI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Mismatches 181; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972;
Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONTAINS 1 F-BOX DOWAIN.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 KKEGDQSISVSAFNIS----SMHNELSGL-----SEKSRQRVEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 ALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.6%; Score 680; DB 1; Length 605; 29.8%; Pred. No. 7.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                           Katayama S., Kitamura K., Toda T.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7118C9379EC5C1F0 CRC64;
                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2000 (Rel. 40, Last annotation update)
F-BOX/WD-REPEAT PROTEIN POFI.
                                                                                 605 AA.
                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50182; WD_REPEATS_2; 7.
PROSITE; PS50194; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
DOMAIN 107 153 F-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F-BOX.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z94864; CAB08168.1; -. InterPro; IPR001680; -.
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Pfam; PF00400; WD40; 7.
                                                                                 STANDARD;
                                                                                                                                                                                                              POF1 OR SPAC57A10.05.C.
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                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
NCBI_TaxID=4896;
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605 AA;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KMFQSWSGPEKLLALDELID-SCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | : || |: || |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 GSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 HTACYKQDLKRTQEINANIAKLP------------LQEQSDIHHII 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 SSSNADIQTQTTRPWKVIYRERFKVESNWRKGHCRIQE-FKGHMDGVLT-LQFNYRLLFT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 LYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGR--RV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRMKRKLDHGSEVRSFSLG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Score 650; DB 1; Length 640;
llarity 26.4%; Pred. No. 1.8e-43;
Conservative 114; Mismatches 197; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> I (IN REF. 1).
5135D4BCA2E1EB97 CRC64;
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WD 2.
WD 4.
WD 5.
WD 6.
WD 8 (POTENTIAL).
M -> I (IN REF. 1).
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                                                                                                                                                                                EMBL; 246861; CAA86905.1; -. EMBL; L26505; AAA96717.1; -.
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72835
                                                                                                                                                                                                                               SGD; S0001308; MET30.
InterPro; IPR001680; -.
Pfan: PF00646; F-box; 1.
Pfan: PF00646; F-box; 1.
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408
449
499
538
538
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640 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                          -i- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-i- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-i- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHGSEVRSFSLGKKPCKVSEYTSTTGL-----VPCSATPTTFGDLRAANG-----Q 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFUR METABOLITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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WD 7.
WD 8.
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                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2000 (Rel. 40, Last annotation update)
SULFUR METABOLITE REPRESSION CONTROL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIRINS: PRO0320; GPROTEINBRPT.
PROSITE; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50082; WD_REPEATS_1; 4.
PROSITE; PS50294; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
DOMAIN 178 224 F-BOX.
                                                                                                                                                                                                                                                                                       678 AA
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Pfam; PF00400; WD40; 6.
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                                                                                                      FNKNFVITSSDDGTVKLW
                                                                                                                                                   617 IGDSECFSGDEFGCVKMY
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15-JUL-1998 (Rel.
01-OCT-2000 (Rel.
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  -----PTGLQE----WLKMFQSWSGPEKLLALDELIDSCE 143
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69URB1, COYT4C6; O9P2S8; O9P2S8;
01-CCT-2000 (Rel. 40, Last sequence update)
FBOX/WD-REPEAT PROYEIN 18 (F-BOX AND WD-REPEATS PROTEIN BETA-TRCP2).
FBXWIB OR FBWIB OR BTRCP2 OR KIAAO696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          400 TKLISGSMDRTIKVWNWRTGECISTYTGHRGGVIGLHFDASILASGSVDKTVKIWNFE-D
                                                                                PIQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLW
                                                                                                     222 HRMCEQHIHRKCKKCGWGLPLLDRKRLRESKREIELRATTWDKGVVGPRSPDASAESPPS
                                                                                                                                                                                                                                               ------KVIK------PGFI---HSPWKSAYIRQHRIDTNWRRGELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and genomic structure of the betaTRCP2 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koike J., Sagara N., Kirikoshi H.,
                                                                                                                                                               ------REKCKEEGIDEPLHIKRR--
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101 GOORRRITSVOP-
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ID FWIB_HI
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WD 6.
WD 6.
WD 7.
MISSING (IN ISOPORM A).
CSVPRSIMLGCANLVESMCALSCLQSMPSVRCL -> NTSV
                                                                                                              -:- FUNCTION: PROBABLY RECCGNIZE AND BINDS TO SOME PROTEINS AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION.
-:- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-:- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AND C (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-:- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 LKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE----LALYVL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVIKP--GFIHSPWKSAYIRQHRIDTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVS 278
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Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNR
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PROSITE; PS50181; FB0X; 1.
PROSITE; PS500678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Ubiquitin conjugation; Repeat; WD_repeat; Alternative splicing.
DOMAIN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 641.5; DB 1;
; Pred. No. 6.5e-43;
89; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF176022, AAF04528.1; -.
EMBL, AB033279; BAA92339.1; -.
EMBL, AB033280; BAA92330.1; -.
EMBL, AB033281; BAA92331.1; -.
EMBL, AB014596; BAA31671.1; ALT_INIT.
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Best Local Similarity 32.1%;
Matches 143; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001680; -. InterPro; IPR001810; -.
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Pfam; PF00400; WD40; 7.
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48
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                                                                                                                                                                  : | ||: | : : || | : ||:|| | :||:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | 
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MEDDLINE-98131628; Pubmed-9653157;
Vallepall1 P.V., Tien D., Kelly T.J.;
"sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml proteins for degradation and stops unwanted diploidization in fission boast ".
                                                                          IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG------QCLQTLQGPNKHQ
316 LIHHNEAVLHLRFSNGLMYTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVYDFDDKY
                                            VVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=972;
Wolf D.A., Jackson P.K.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
WD-REPEAT PROTEIN POP2 (PROTECLYSIS FACTOR SUDI)
POP2 OR SUDI OR SPAC4D7.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 95:8159-8164(1998).
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Pfam; PF00400; WD40; 6.
PRIMYS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; PBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_2; 6.
                                                                                                                                                                                                                             SAVTCLQFNKNFVITSSDDGTVKLWD 532
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EMBL; AF04515; AAC39496.1; --
EMBL; 298602; CAB11275.1; --
InterPro; IPR001680; --
InterPro; IPR001810; --
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014170;
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                                                                                                                                                                                                                                                                                                85 LKHSCTPSFLRKFNESIENVSYKCLDHSPPDSVPGDFSISLVPQRNFLYSHSSLPPKIIS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCLHTLQGHTNRVYSLQFDGIH---VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMEL 471
                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 KDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 IDRNNRIKLDNSISSNSDNFPPSPKVDTSNTVSPGSKPISE-----DLEDLNLQSIVQ-
                                                                                                                                                                                                                                                                                                                                                                                                           106 RITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISL
                                                                                                                                                                                                                                                                                                                                                                                                                                              --TFEDLPEGIOSY-------AFFQLLRSCNRQSMRLLLNECEPLLKKDILSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPKELALYVLSFLEPKDLLQAAQTCRYW-RILAEDNLLWREKCKEEGI---DEPLHIKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LPFSIVOSILLNLDIHSFLSCRLVSPTWNRILDVHTSYWKHMFSLFGFQINENDWKYANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------ETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETE
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 80.3 KDA TRP-ASP REPEATS CONTAINING PROTEIN K10B2.1
                                                                                                                                                                                                                                Indels 116;
                                                                                                                                                                                         20.4%; Score 641; DB 1; Length 703; ilarity 27.3%; Pred. No. 1e-42; Conservative 111; Mismatches 248; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDF
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                                                                                                                                        0336A0568C152396 CRC64;
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                  F-BOX
                              WD 2.
WD 3.
WD 4.
WD 5.
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                                                                                                                                        703 AA;
                                                                                                                                                                                                              Similarity
                                389
429
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                                                                                                                                                                                                                            Matches 178;
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Q09990;
                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                        SEQUENCE
 Repeat;
DOMAIN
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                                                                 REPEAT
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NCBI_TaxID=6239;

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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 603482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pagano M.
                                          RESULT 9
FW1A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSEHEQLDFMDKIVHRLSHYQLGKVDNFIRPMLQRDFISNLPAHLVELIL-FNVNSDSLK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AAQ-----TC----RYWRILAEDNL----LW--------------REKCKE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 FNYD--VNIKRDKLDQLILMHVFYSKLYPKIIRDIHNIDNNWKRGNYKMTRINCQSENSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: | | :: | | |: SCEEVSTSWRCALARGQHWKKLIEKNVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 EGIDEPLHIKRRKVIKPGFIHSPWKSAY -- - IRQ - HRIDTNWRRGELKSPKV - LKGHDDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 VITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRVWDVETGECIKTLIHHCEAVLHLRFANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVG
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DNTIRLWDIHSGVCLRVLEGHBELVRCIRFDEKRIVSGAYDGKIKVWDLQAALDPRALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MD 1.
WD 2.
WD 3.
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WD 6.
WD 6.
WD 7.
WD 7.
WD 6.
WD 7.
WD 7.
POLY - ALA.
                                                                                                                 -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                             Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 EICLCSLV---QHTGRVFRLQFDDFQIVSSSHDDTILIWD 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.3%; Score 639.5; DB 1; 33.5%; Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- CLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD repeat
                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0320; GPROTEINBRPT.
PROSITE; PS50181; FBCX; 1.
PROSITE; PS500678; WD_REPEATS_1; 5.
PROSITE; PS50083; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80320 MW;
                                                                                                                                                                                                                                                                                                                                  EMBL; U28730; AAA68258.1; -.
                                                                                                                                                                                                                                                                                                                                                       WormPep; K10B2.1; CE02008.
InterPro; IPR001680; -.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.35
Best Local Similarity 33.55
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
364
407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           701 AA;
                                                          STRAIN=BRISTOL N2;
                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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-1- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA

(PIKAPPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR

UBIQUITINHATION AND DEGRADATION.

-1- SUBUNIT: PART OF A SCF (SKPI-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC.

-1- ALTERNATIVE PRODUCTS: 2 ISOPOMAS; 1 (SHOWN HERE) AND 2; ARE

PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V., Thomas D., Strebel K., Benarous R.; A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif."; Mol. Cell 1:565-574(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with phosphorylated destruction motifs in I-kappa-B-alpha and beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harper J.W.;
"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
FWIA_HUMAN STANDARD; PRT; 605 AA.
09Y2097; 09Y213;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
F-BOX-WID-REPEAT PROTEIN IB (F-BOX AND WD-REPEATS PROTEIN BETA-TRCP)
FBXWIA OR FBWIA OR BIRCP OR BIRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M., Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.; "Identification of the receptor component of the IkappaBalpha-
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-99075339; PubMed-985996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98325370; PubMed-9660940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubiquitin ligase.";
Nature 396:590-594(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001680; -. InterPro; IPR001810; -. Pfam; PF00646; F-box; 1. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA74572.
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                                                                                                                                                                                                                                                                                                                                                                                         E-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRIDTN 246
                                                                                                                                                                                                                                                                                                                                                                                                                     306 VWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGQG----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQ 152
                                                                                                                                                                                                                                                                            113 NGTSSMIVPKORKLSASYEKEKEL -- CVKYFEQWSESDQVEFVEHLISOMCHYQHGHINS 170
                                                                                                                                                                                                                                                                                                                                                           231 RMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESN 285
                                                                                                                                                                                                                                                                                                                                                                              WRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                        346 VLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 RVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFWVKVWDPETETCLHTLQGH 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 TNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNAD 482
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                      NSSEREDCHNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA----TPTTFGDLRAA 97
                                                                                                                                                                                                                                                                                                           Q91854; P70037; P70038; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 01-OCT-2000 (Rel. 36, Last annotation update) 01-OCT-2000 (Rel. 40, Last annotation update) BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN). FBXM1 OR BTRCP. Senopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Kenopus.
                                                                                                                                                                                                                                                                                               153 VIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD
                                            conjugation; Repeat; WD repeat; Alternative splicing. 190 228 F-BOX. 301 338 WD 1. 378 WD 2. 381 418 WD 3. 424 461 WD 4.
                                                                                                                                                                              Length 605;
                                                                                                                                                                           20.3%; Score 638; DB 1; Length 60 30.8%; Pred. No. 1.4e-42; ive 92; Mismatches 209; Indels
                                                                                                                                      MISSING (IN ISOFORM 2).
4C67F3B7E400FD37 CRC64;
                 PS00678; WD_REPEATS_1; 6.
PS50082; WD_REPEATS_2; 7.
PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                   WD 1.
WD 2.
WD 4.
WD 5.
GPROTEINBRPT
                                                                                                                                                68866 MW;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                         553
17
605 AA;
                                                                                                                                                                                       Similarity
          PS50181;
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381
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464
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                                                                                                                                                                                               166;
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                                                Ubiquitin
                                                                                                                                                                            Query Match
                           PROSITE;
PROSITE;
                                                                                                                                       VARSPLIC
                                                                                                                                               SEQUENCE
                  PROSITE
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the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ջ
                                                                                                                                                                                                                                                                     differential display PCR.";
Dev. Genet. 19:190-198(1996).
-!- FUNCTION: PROBABLY RECOGNIZE AND BINDS TO SOME PHOSPHARYLATED
PROTEINS AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION.
-!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLP----KE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLKPMLQRDFITALPARGLDH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRSFSLGKKPCKVSEYTSTTGLVPCSATPT---TFGDLRAANGQGQQ---RRRITSVQPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-MATURED OCCYTES. THE LEWEL CHANGES WERY LITTLE BYEN AFFER XYGOTIC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSTION. IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ţ
MEDLINE-93330289; PubMed-8393141;
Spevak W., Keiper B.D., Stratowa C., Castanon M.J.;
"Saccharomyces cerevisiae cdc15 mutants arrested at a late stage i
anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein
with beta-transducin repeats.";
Mol. Cell. Biol. 13:4953-4966(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TADPOLE EMBRYO.
--- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
--- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
--- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
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                                                                                                                                                                           SEQUENCE OF 302-518 FROM N.A.
MEDILNE-97109804; PubMed-8952061;
Hudson J.W., Alarcon V.B., Elinaon R.P.;
"Identification of new localized RNAs in the Xenopus oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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WD 2.
WD 3.
WD 4.
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WD 7.
GEM -> BFR (IN REF. 2).
GLA -> AAH (IN REF. 2).
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31.1%; Pred. No. 2.2e-42;
1ve 90; Mismatches 214;
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DOMAIN 119 157 F-BOX.
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PROSITE; PS00678; WD_REPEATS_1; 6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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Matches 161; Conservative
                                                                                                                                                    [2]
SEQUENCE OF 302-518 FROM
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Pfam; PF00400; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN MAINTENANCE OF PLOIDY THROUGH PROTEASOME
DEPENDENT DEGRADATION OF CDX INHIBITOR RUMI AND S-PHASE INITIATOR
CDC18. FUNCTIONS AS A RECOGNITION FACTOR FOR RUMI AND CDC18, WHICH
ARE SUBSEQUENTLY UBIQUITINATED AND TARGETED TO THE 26S PROTEASOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Fission yeast WD-repeat protein popl regulates genome ploidy through ubiquitin-proteasome-mediated degradation of the CDK inhibitor Ruml and the S-phase initiator Cdc18."; Genes Dev. 11:1548-1560(1997).
                                                                                                                                                                                                  327 VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMGHV 383
                                                                                                                                                                                                                                                                     443
                                                                                                                                                                                                                                                                                     ||| | :| : :|| : | :||:| | :||:| | AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN 415
                                                                         K-----VIKPGFIHSPWKSAY----IRQ--HRIDTNWRRGELKSPKV-LKGHDDHVI 266
                                                                                                        235
                                                                                                                                                                                                                       444 SIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG------Q 494
                                                                                                                                                                                                                                                                                                                                                             416 TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTL 475
                                                                                                                                                       ----EGIDEPLHIKRR
                                          121 IAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAE----RR
                                                                                                     176 GWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGV
                                                                                                                                         TCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
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SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
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Wakaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
             LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKE---
                                                                                                                                                                                                                                                                                                                                                                                            495 CLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWD 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
WD-REPEAT PROTEIN POP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 AA
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SEQUENCE FROM N.A.
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P87060;
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357 DSKIRTMCLEQSLSACAIMKR------VYFRHFNLRERW----LHAPEKIK 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 SIHPSNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 GSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNA--DSTVKIWDIKTGQCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 AGTDAKIRIWNLESGELLQTLHGHSNLVSQVTFNQNILVSASAPPDTSLRVWDLNTGSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 QKNFLTGFPAEITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 G----HDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----REKCKEEGIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHL-------HEKR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 124;
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WD 2.
WD 3.
WD 4.
WD 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%; Score 620; DB 1; 27.5%; Pred. No. 5.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            llarity 27.5%; Pred. No. 5.2e Conservative 100; Mismatches
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                                                                                                                                                                      PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FBOX, 1.
PROSITE; PS50082; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Bepeat; WD_repeat. 345 F-BOX.
send an email to license@isb-sib.ch)
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687 WI
87816 MW;
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P07834;
01-AUG-1988 (Rel. 08, Created)
                                      EMBL; Y08391; CAA69671.1; -.
EMBL; AL022103; CAA17898.1; -
InterPro; IPR001680; -.
Interpro; IPR01810; -.
Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 6.
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484
575
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775 AA;
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es 153; Conserv
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CC4_YEAST
ID CC4_YE
AC P07834
DT 01-AUG
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Matches
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16;

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Query Match
                                      Best Local
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                                                                                                                     MEDLINE-88011240; PubMed-3309335;
Yochem J., Byers B.;
"Structural comparison of the yeast cell division cycle gene CDC4 and
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-579 FROM N.A.

STRAIN-S288C / AB972;

Barrell B.G., Churcher C., Rajandream M.A.;

Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INTITATION OF DNA

REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM THE
POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTAL-HTBL LOCUS
TRANSCRIPTION ACTIVATION.
                                                                                                                                                                                                                             Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eti T., Fill T., Analysis of the nucleotide sequence of chromosome VI from
                                                           Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS I F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> E (IN REF. 1).
0348F2F8FA78F3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; WD
 Last sequence update)
Last annotation update)
                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 5.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell division; Mitosis; Sporulation;
DOMAIN 272 319 F-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD 2.
WD 2.
WD 3.
WD 5.
WD 6.
                                                                                                                                                                                                       STRAIN-S288C / AB972;
MEDLINE-95400292; PubMed 07670463;
            01-OCT-2000 (Rel. 40, Last annot
CELL DIVISION CONTROL PROTEIN 4.
CDC4 OR YFL009W.
                                                                                                                                                          related pseudogene.";
Mol. Biol. 195:233-245(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X05625; CAA29113.1; -.
EMBL; D50617; BAA09229.1; -.
EMBL; D31600; BAA06495.1; -.
EMBL; Z46255; CAA86341.1; -.
PIR; A26867; A26867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86089 MW;
                                                                                                                                                                                                                                                                                        Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; 1.
Pfam; PF00400; wD40; 6.
                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.
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32,
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779 AA;
                                                                                                        SEQUENCE FROM N.A.
 01-NOV-1995 (Rel.
                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                   NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461
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                                                                                                                       LDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYW- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E----TGNC------IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDI 490
                                                                                                                                                         194 RILAEDNLLWREKCKEEGIDEP-----LHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWR 248
                                                                                                                                                                                                                                                                                                       KIIRKSTSLWKKLLISENFVSPKGFNSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNW- 365
                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRGHMASVRTVSGHGN 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ANDYSRKFSYHHINLSAITTFYVSDNILVSGSEN-QFNIYNLRSGKLVHANILKDA--- 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 RGELKSPK-----VLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGVWS-SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHE----KRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 KTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLELES OF THE UNLINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta homologous domain.";
Gene 162:135-139(1995).
--- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED
                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Podospora.
NCBL_TaxID=5145;
   Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
                                                             Indels
19.7%; Score 618.5; DB 1;
llarity 29.6%; Pred. No. 6.9e-41;
Conservative 105; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2000 (Rel. 40, Last annotation update)
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                 Similarity
                                                             Matches 152;
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23;
   oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                   590 PESLEEIVKLCGSFLIIRERTVYFVHQSAKDFLLGTASDKASNKASQEAFELVFPTGIED 649
                                                                                                                                                                                                                                                                                                                                                                            M-------MQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYW------ 193
                                                                                                                                                                                                                                                                                                                                                                                          246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VIKPGF-------IHSPWKSAYIRQHR------IDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 IAIVRDGYRFALSYRMIIEKAPLQAYTSALVFAPTDSMIKKIFKKEEPGWISTISVVEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRRGELKSPKVLKGHDDHVIT-CLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWS---SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHE--KRVVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDATLRVWDIETGQCLHVLMGHVAAVRCVQY - - DGRRVVSGAYDFWVKVWDPETETCLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 LQGHTNRVYSLQF---DGIHVVSGSLDTSIRVMDVETGNCIHTLTGH----QSLTSGMELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 DNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVKL
                                                                                                                                                                                                                                                                                                                                                                                                                        -------EPL--HIKRRK-
                                                                                                                                                                                                                                                                                                             Indels 137;
                                                                                                                                                                                                                                                                                       Length 1356;
                                                                                                                                                                                                                                                        965FB319844E0651 CRC64;
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                                                                                                                                                                                                                                                                                      Score 582.5; DB 1;
Pred. No. 1e-37;
85; Mismatches 193;
                                                                                                                                  GTP (POTENTIAL).
   removed
                                                    InterPro; IPR001680; -.
Pfam; PF00400; WD40; 10.
PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS00678; WD_REPEATS.1; 10.
PROSITE; PS50082; WD_REPEATS.2; 10.
PROSITE; PS50294; WD_REPEATS.2; 10.
                       or send an email to license@isb-sib.ch)
            entities requires a license agreement
modified and this statement is not
                                                                                                                                            888888888
                                                                                                                      Repeat; WD repeat.
                                                                                                                                                                                                                                                                                      Query Match 18.5%;
Best Local Similarity 28.9%;
Matches 169; Conservative 8
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                                           EMBL; L28125; AAA85775.1; -
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REPEAT
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SCO2_NEUCR

RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                          STRAIN-74-0R23-1A;

MEDLINE-9541499; PubMed=7724564;

Kumar A., Paietta J.V.;

Kumar A., Paietta J.V.;

"The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a protein with beta-transducin repeats.";

Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).

-! FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.

-! INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.

-! SIMILARITY: CONTAINS 8 WD REPRATS (TRP-ASP DOMAINS).

-! SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 RITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDS-CEPTQVKHMMQVIEPQFQRDFIS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLW------REKCKEEGIDEPL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ::|:: | |
189 LERKKLRNYTRQRQLAKGGPQGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 173;
                                                                                       Bukaryota; Fung1: Ascomycota; Pez1zomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7473859C99F1B028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 576.5; DB
Pred. No. 1.1e-37
                                     Last sequence update)
Last annotation update)
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repeat.
 650 AA
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WD 2.
WD 3.
WD 4.
WD 5.
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                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq)
01-CCT-2000 (Rel. 40, Last and
SULFUR CONTROLLER-2 (SCON2).
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72189 MW;
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18.3%;
Best Local Similarity 26.3%;
Matches 155; Conservative 8.
 STANDARD;
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                                                                                     Neurospora crassa.
                                                                                                                                                SEQUENCE FROM N.A.
SCO2_NEUCR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelabbsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clancy C. E., Mondoza M.G., Nalsmith T.V., Kolman M.F., Egelhoff T.T.;

"Identification of a protein kinase from Dictyostelium with homology
T to the novel catalytic domain of myosin heavy chain kinase A.";
J. Biol. Chem. 272:11812-11815(1997).

- FUNCTION: PHOSPHORYLATES THREONINE IN THE C-TERMINAL TAIL REGION
OF WYOSIN II HEAVY CHAIN. THIS PHOSPHORYLATION IS CRITICAL IN
REGULATIC ACTIVITY: ATP + [MYOSIN HEAVY-CHAIN] = ADP +
[MYOSIN HEAVY-CHAIN] PHOSPHATE.

- I CATALYTIC CONSISTS OF AN WITERMINAL DOMAIN MITH SEVEN WD REPEATS.

- DOMAIN: CONSISTS OF AN GREENING DOMAIN WITH SEVEN WD REPEATS.

- SIMILARITY: GOWAINS 7 WD REPEATS (TRP-ASP DOMAINS).

- SIMILARITY: BELONGS TO THE MHCK / EF-2 PROTEIN KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                435
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                       249 MAAAEASKAVTQPKTRSWKAVYRDRWQVSYNWKNSRYKL-SVLKGHENGV-TCLQLDDNI 306
                                                                                                                                                       IHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYD--G 393
                                                                                                                                                                                 431
-----FIHSP----WKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                546 LPPRYFMTGGLDSTMRLWDSATGRCLRTLFGHLEGVWSLAG-----DTIRVISGANDGMV 600
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                                                                                                                                                                                                                                                                         RIVFSASDDTTIKLWDLDTROVIRTYEGHVGHVQQVLILPPEYEPDEEVLNGASQDNQDA
                                                                                                                                                                                                                                                                                                              486 MSVSSGGSGSPSMSHAQIERAGSPGSHSSSHNLLPSSLPSGDEDVRHLYGSAFVADESRP
                                                                                                                                                                                                                                                                                                                                                                                            ----VVSGSLDTSIRVWDVETGNCIHTLTGH----QSLTSGMELKDNI-LVSGNADSTV
                                                                         276 IVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                     RRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF----
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DictyDb; DD01087; mhkB.
InterPro; IPR001680; -.
Pfam: PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS00678; WD_REPEATS_1; 5.
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STRAIN~AX3;
MEDLINE~97277316; PubMed∻9115238;
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                                                                                                                                                                                                                                                                                    DRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMG 381
                                                                                                                                                                                                                                                                                                                          HVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSL 441
                                                                                                                                                                                  Gaps
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
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                                                                                                                                                                                  36;
                                                                                                                                                               Length 732
                                                                                                                                                              16.4%; Score 516; DB 1; Length 73 34.0%; Pred. No. 7.2e-33; ive 72; Mismatches 111; Indels
                                                                                                                                 A7233C4BD56D408B CRC64;
                                         (POTENTIAL)
                                                                                                                                                                                                     231 SPWKSAYIRQ--HRIDINWRRGELKS-----PKVL--
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                                        ATP (POTE POLY-ASN. WD 1. WD 3. WD 4. WD 5. WD 5. WD 6. WD 7.
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                                                                                                                                  83167 MW;
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Matches 113; Conservative
                                         303
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Search completed: September 25, 2001, 14:45:03 Job time: 208 sec

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OM protein

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Sequence:

Searched:

Database

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096698 drosophila
0972a6 mus musculu
0972a6 mus musculu
094073 homo sapien
096792 arabidopsis
090703 drosophila
090713 dictyostell
09008 rattus morv
061385 strongyloce
04560 homo sapien
055039 mus musculu
094878 drosophila
093531 xenopus lae
093531 xenopus lae
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Q9vp10 drosophila
Q9vyq9 drosophila
Q9vyq9 drosophila
Q9713 schizosacch
Q9713 schizosacch
Q9hal homo sapien
Q9nxz homo sapien
Q9nxz homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A ISOGAL T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
A Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
A Natsunawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
A Matsunawa T., Nagahari K., Sasaki K., Yamamoto J., Wakamatsu A.,
A Nakamura Y., Nagahari K., Mawal Y., Sasaki N.;
Bakamura Y., Nagahari K., Sasaki N.;
C Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
B NEDO human CDNA sequencing project."; Sasaki N.;
InterPro; IPR00180; Ot the EMBL/GenBank/DDBJ databases.
B InterPro; IPR00180; Othe EMBL/GenBank/DDBJ databases.
B NED TROUGHOUS (PLOX: 1.)
B Pfam: PF00400; WD40; 7.
B Pfam: PF00400; WD40; 7.
B PROSITE; PS00678; WD_REPEATS; UNKNOWN_S.
B PROSITE; PS00678; WD_REPEATS; UNKNOWN_S.
B SEQUENCE 553 AA; 62280 MW; CAR829C221986A3F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ11071 FIS, CLONE PLACE1004937, MODERATELY SIMILAR TO SEL-10
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 91.9%; Score 2889; DB 4; Length 553; Best Local Similarity 99.8%; Pred. No. 2.8e-237; Matches 540; Conservative 1; Mismatches 0; Indels
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Q9R2A6
074855
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Q9FGS2
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09WUC8
061385
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09V878
09USN3
09USN3
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09V8V0
09SQDQ
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 SEQUENCE FROM N.A.
TISSUE-PLACENTA;
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09z159 mus musculu
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09r197 mus musculu
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09r7v1 schizosophila
09p7v1 schizosacch
09pfx1 dictyosteli
09prx7 homo sapien
09prs gallus gall
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Q9vzf4 drosophila
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                    Compugen Ltd.
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Copyright (c) 1993 - 2000 Comp
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    protein search, using sw model

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RA Adams W.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holf R.A.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Change M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Rorkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabriellan A.E., Gargy N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  588
               MHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVW 408
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                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoā; Arthropoda; Trācheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID÷7727;
SVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPK 168
                                                                           IHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVW
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Last annotation update)
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13,
16,
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Mulahina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.K., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

She B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,

She Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Weissenbach J.,

RA Hiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT The genome sequence of Drosophila melanogaster.";

REMBI, AEO03480; AAG22246.1; -
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Pred. No. 1.8e-166;
I; Mismatches 98;
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Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS00181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS; 5.
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32.7%;
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SEQUENCE FROM N.A.
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Best Local S
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                      ### Hubbard B.J.A., Wu G., Kitajewski, J., Greenwald I.;

# Hubbard B.J.A., Wu G., Kitajewski, J., Greenwald I.;

# sel-10, a negative regulator of lin-12 activity in Caenorhabditis

# degans, encodes a member of the CDC4 family of proteins.";

# RMBL; APO20788; AAC47809.1; -.

# InterPro: IPR000412; -.

# InterPro: IPR000412; -.

# InterPro: IPR001810; -.

# Ream; PF00440; WD40; 7.

# Pfam; PF00446; F-box; I.

# PRINTS; PR00490; ABC2_MEMBRANE; UNKNOWN_I.

# PROSITE; PS50181; FBOX; I.

# PROSITE; PS50181; FBOX; I.

# PROSITE; PS00890; ABC2_MEMBRANE; UNKNOWN_S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 QPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKEL 170
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                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
SSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | | : | | : | | : | DNGEE-SSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPR------
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                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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85; Mismatches
                                                                                                                                                                                                                                     587
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SEQUENCE FROM N.A.
MEDLINE-98051191; PubMed-9389650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat.
587 AA; 65311 MW;
                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 262; Conserv
                                                                                                              1314 LDFDVE 1319
                                                                                 LDFDVD 587
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522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein LIN-23 functions
                                                                                                                                                                     -VVSGSLDTSIRVWDV---ETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIK
                                                                                      TGQCLQTLQGPNKHQSAVTCLQ-FNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 RDNTIKIWDRKDYSCSRILSGHTGSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 GHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCEAVLHLRFANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVGHRAAVNVVDFDDRYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 CEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQ-----TC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGFIHSPWKSAY ---IRQ-HRIDTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28037.1; -.
75916 MW; BF3E9AF51F12ECCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Pred. No. 8.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kipreos E.T., Gohel S.P., Hedgecock E.M.;
"The Caenorhabditis elegans F-box/WD-repeat it olimit cell division during development.";
Development 127:5071-5082(2000).
SEQUENCE 665 AA; 75916 MW; BF3E9AF51F1PF
                                                                                                                                                                                                                             GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFD 585
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                        Nakayama K.-i.;
                                                                                                    544 WD 545
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Matches 164;
                                                                               WD 532
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                                                                                                                                                              090UI5;
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SINDMASSTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ::| |||||:|| :| :||:::
132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DINWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDINE-991445465; PubMed-9990853; Spencer E., Jiang J., Chen Z.J.; "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 KLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 KCKE------EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGLV------PCSATPTTFGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.2%; Score 635; DB 11; Length 569; 30.3%; Pred. No. 1.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                BC7C7A44815BED96 CRC64;
                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN.
                                                                                                                 569 AA
                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS50181; FBOX; 1.
SMO320; WD_REPEATS; UNKNOWN_6.
SMART; WD CEPEAT.
REPEAT; WD CEPEAT.
SEQUENCE 569 AA; 65047 MW; BC7C7A448
                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                 PRT;
                                 509 VICLQFNKNFVITSSDDGTVKLWD 532
                                            | |||| ||| || ||| ||| ||| ||| ||| || VFRLQFDDFQIVSSSHDDTILIWD 500
                                                                                                                                                                                                                                                                                                 Genes Dev. 13:284'294(1999).
EMBL; AF112979; AAD04181.1;
InterPro; IPR001680; -.
Interpro; IPR001810; -.
Pfam; PF00400; Wb40; 7.
Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 164; Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                    musculus (Mouse)
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                                                                                                                                                                                                                     NCBI_TaxID=10090;
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480 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL 530
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Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
"Identification of the receptor component of the IkappaBalpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Ubiquitin-dependent degradation of IkappaBalpha is mediated by ubiquitin ligase Skpl/Cul 1/F-box protein FWD1."; Proc. Natl. Acad. Sci. U.S.A. 96:3659-3863(1999).
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Nature 396:590-594(1998).

RAULA AF091823. AAD08701.1;

EMBL; AF099323. AAD08701.1;

Interpro; IPR001680; -...

Interpro; IPR001680; -...

Fam; PF00406, WD40; 7...

Pfam; PF00406, WD40; 7...

PRINTS; PS00466; F-Dox; 1...

PROSITE; PS00678; WD_REPEATS; UNKNOWN_6.

SARRY; SAN0320; WD40; 1...

RARRY; SAN0320; WD40; 1...

SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2001 (TrEMBLrel. 16, Last annotation update)
UBIQUITIN LIGASE FWDI.
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PROSITE; PS00678; WD_REPEATS; UNKNOWN_S.
SMART; SM00320; WD40; 1.
Repeat; WD repeat.
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Nature 391.493.496(1998).
BEBL; AF032878; ARC38852.1; -
FlyBase; FBgn0023423; slmb.
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InterPro; IPR001810; -.
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT.
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                                                                                                             362
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LIERMVRTDSLWRGLAE----RRGWGQYLFKNKPPDENAPPNSFYRALYPKIIQDIETI
                                                         QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Winston J., Elledge S.J., Harper J.W.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, **AP110396; **AP40125.1; -.
InterPro; IPR001680; -.
InterPro; IPR001810; -.
Pfam; PF00400; WI40; 7.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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PRINTS; PR00320; GRROTEINBRPT.
PROSITE; PS006181; FBOX; 1.
SMART; SM00320; WD_REPEATS; UNKNOWN_6.
Repeat; WD repeat.
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hes 163; Conservative
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Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidea; Drosophila.
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    SLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE----KCKEEGIDEP 215
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|| | | : :||:||:||:||: || TGSVLCLQYDERVIITGSSDSTVRVWDVNAGEMLDTLTHHCEAVLHLRFNNGMAYTCSKD
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.larity 30.6%; Pred. No. 3.9e-44;
Conservative 91; Mismatches 190;
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REALINE—SCUENCE FROM N.A.

REALINE—SCUENCE FROM N.A.

RADILINE—20196006; PubMed 0.10731132;

RADILINE—20196006; PubMed 0.10731136;

RADILINE—20196006;

RADILINE—20196006;

RADILINE—20196006;

RADILINE—2019606;

RADILINE—
                                                                                                                                                                                                     437 VSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDI----- 490
                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-20245299; PubMed-10781936;
MIDCLINE-20245299; PubMed-10781936;
Miletich I., Limbourg-Bouchon B.;
"Drosophila null slimb clones transiently deregulate Hedgehog-independent transcription of wingless in all limb discs, and induce decapentaplegic transcription linked to imaginal disc regeneration.";
Mech. Dev. 93:15-26(2000).
EMBL; AF022924; AAF558551; ..
EMBL; AF22924; AAF63214.1; ..
EMBL; AF229243; AAF63213.1; ..
Flybase; FBG00024433; slmb.
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Wooden T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
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30.6%; Pred. No. 3.9e-44;
Live 92; Mismatches 189;
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PROSTTE; PS50181; FBOX; 1.
PROSTTE; PS00678; WD_REPEATS; ESMART; SM00256; FBOX; 1.
Repeat; WD_repeat.
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Matches 146; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEG--IDEPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LKSPKVLKGHDDHV-----ITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 LVSTFNNPSIRFPADQDFRATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTGGVWSSQM--RDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRDATLRVWDIETGQ----CLHVLMGHVAAVRCVQYDGRR--VVSGAYDFMVKVWDPETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HIKRRKVIKP-GFIHSP-------WKSAYIRQHRIDTNWRRGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCIRITHAHQRGIACAQYNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFND
                                                                                                                                                                                                                                                                                                                                 McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy Jones L., McNeil A., Harris D.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL136538; CA866464.1; -. InterPro; IPR001680; -. InterPro; IPR001810; -. Pfam; PF00400; WD40; 7. Pfam; PF00460; WD40; 7. Pfam; PF004646; F-box: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEF34D4EFFBC2E10 CRC64;
                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 533; DB 3; L425.8%; Pred. No. 5.4e-37; Live 91; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIMTS; PR00320; GREOTEINBRPT.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58256 MW;
                                  01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.0%;
Best Local Similarity 25.8%;
Matches 140; Conservative
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                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 AA;
                                                                                                           WD-REPEAT PROTEIN.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTG 536
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503 ISTSTSSSSSILNNFSI-----NIILPINLIILIFREIKPNFVNTLSRVCKHWKQ 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 TSTIGLVPCSATPTTFGDLRAANGQGQQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLAL 135
                                                                                                                                                                                                                                                                                                                                                                                          Chung C.Y., Reddy T.B.K., Zhou K., Firtel R.A.;
"A novel, putative MEK kinase controls developmental timing and spatial patterning in Dictyostellum and is regulated by ubiquitingenes Dev. 12:3564-3578(1998).
"- SIMTIANTIY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AR093689; AAC97114.1; -
InterPro; IPR001019; -.
InterPro; IPR0011845; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 DELIDSCEPTOVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Kinase; Repeat; Serine/threonine-protein kinase;
Transferase; Tyrosine-protein kinase; WD repeat.
SEQUENCE 942 AA; 105796 MW; C9E4928A8C7C68F7 CRC64;
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                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                   Last sequence update)
Last annotation update)
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Pfam; PF00646; F-box; 1.

PRINTS; PR001320; GPROTEINBRPT.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS5011; PROTEIN_KINASE_ATP; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; WD_REPEALS; UNKNOWN_4.
942
                                                      Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99051319; PubMed=9832508;
                                                   9 (TrEMBLrel. 10, 0
9 (TrEMBLrel. 10, 1
1 (TrEMBLrel. 16, 1
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InterPro; IPR001810; -.
InterPro; IPR002290; -.
Pfam; PP00069; pkinase; 1.
PRELIMINARY;
                                                   01-MAY-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 FTCKIFSLKTKKTLFTYTNHQEAVTCINYLGDVENKCITSSLDKTIQLWDAETGSCLSTL 777
                                                                                                                                                                                                                                              258 LKGHDDHVITCLQFC--GNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGV----WSSQM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SNLLVSASDDKTLKIMDVSSGKCLKTLKGHSNIVFCCNFNPQSNLIVSGSFDESVRIWD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IETGQCLHVLMGHVAAVRCVQY - - DGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 S-LQF--DGIHVVSGSLDTSIRVMDVETGNCIHTLIGHQ------SLTSGMELKDN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 WIVSGSEDNLVYIWNLQTKEIVQKLQG---HTDVVISTACHPTENIIASAALENDKTIKL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota Suzuki Y., Obayashi M., Mishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ARODO552; BAA91248.1; -...InterPro; IPR001680; -...InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 LKDNILVSGNADSTVKIWDIKTGQCLQT-LQGPNKHQSAVTCLQFNKNFVITSSDDGTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 ILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAV--TCLQFNKNFVITSS--DDGTVKL
                                                                 QGHTNRVYSLQFDGI-----H-VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGME
                                                                                                           :||| :| : | : | | RGHIGGIYCVKTDQVATHGNGYNHLVVSASVDKTSNVWDJRSSSKVRSFIQHTEDVLCCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%; Score 461; DB 4; Length 334; 33.9%; Pred. No. 4e-31; Live 68; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat.
334 Aa; 36588 MW; 4BF30914A2250286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NWX7;
01-0CT-2000 (TYEMBLrel. 15, Created)
01-0CT-2000 (TYEMBLrel. 15, Last sequence update)
01-0CT-2001 (TYEMBLrel. 16, Last annotation update)
CDNA FLJ20545 FTS, CLONE KAT11476.
                                                                                                                                                                                                                                                                                                                                               LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLV 565
                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00319; GPROTEINB.
PRINTS; PR00320; GPROTEINBRPT.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_4.
Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 102; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
Q9NWX7
                                                                     420
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                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 GFIHSPWKSAYIRQHRI------DTNWRRGELKSPK-----VLKGHD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHTGKLLASC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 GGKFILSCADDKTLRVWDFKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDQTVK 405
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB-ALPHA SUBUNIT.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reiner O.; Shundin.

Technical Control of the chicken homolog of LIS1.";

Characterization of the chicken homolog of LIS1.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF113946; AAF18938.1; -.

REMBL, AF113946; WD401; J.

REMBL, AF113946; WD401; J.

REMBL, AF113946; WD-REPEATS; UNKNOWN_S.

REMBL, AF113946; WD-REPEATS; UNKNOWN_S.

REPEAT; WD repeat, WD Repeat; WD repeat, W
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29.9%; Pred. No. 4e-29;
Live 63; Mismatches 133; Indels
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9031;
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VWECR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 LWDLK 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q9PTR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q9GL51
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                                                SEQUENCE FROM N.A. Magasaka T., Boulday G., Coupel S., Coulon F., Tesson L., Magasaka T., Soulillou J.-P., Charreau B.; Cloning of porcine PAF-AH Ib-alpha cDNA and expression in endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

ILSOGI-PLACENTA;

ISOGIA T., Ota T., Hayashi K., Suqiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Nishikawa T., Magai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosolif T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK002149; BAA92110.1;
                                                                                                                                                                                                                                                                                                                                                                                263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 GFIHSPWKSAYIRQHRI------DINWRRGELKSPK------VLKGHD 262
                                                                                                                                                                                                                                                                                                                                                49 GLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPKEWIPRPPEKYALSGHR 108
                                                                                                                                                                                                                                                                                                                                                                                                                  109 SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKWMDVSTGMCLMTLVGHDNWVRGVLFHS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 GGKFILSCADDKTLRVWDYKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDQTVK 405
                                                                                                                                                                                                                                                                               60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ11287 FIS, CLONE PLACE1009596, WEAKLY SIMILAR TO VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 TFTGHREWVRMVRPNQDGTLIASCSNDQTVRVWVATKECKAELREHEHVVECISWAPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           13.9%; Score 436; DB 6; Length 410; 29.9%; Pred. No. 7.1e-29;
                                                                                                                                                                                                                                                                             63; Mismatches 133; Indels
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF319658; AAG33867.1; -.
                                                                                                                                                                                           410 AA; 46654 MW; AO8DAFCD8B8B2719 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 AA
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                           Best Local Similarity
Matches 109; Conserv
                 NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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406 VWECR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530 LWDLK 534
                                                                                                                                                                       Hydrolase.
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                           Query Match
                                                                                                                    cells."
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 SOW RET REPRES
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312 RDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLH--EKRVVSGSRDATLRVWD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 IETGQCLHVLMGHVAAVRCVQYD - GRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVY 427
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              258 LKGHDDHVITCLQFC--GNRIVSGSDDNTLKVWSAVTGKCLRTLVGH----TGGVWSSQM 311
                                                                                                                                                                                                                                                                                                                                                                              326 WIVSGSEDNL/YIWNLQTKEIVQKLQGHTDVVISAAC-HPTENLIASAALENDKTIKLW 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 ILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSS--DDGTVKLW
                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                    Length 330;
                                                                                                                                                                            F78396D3B5B716CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-LQF--DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQ-----
                                                                                                                                                                                                                                             Query Match 13.6%; Score 426; DB 4; Best Local Similarity 31.8%; Pred. No. 3.7e-28; Matches 95; Conservative 71; Mismatches 99
                                                                                                                               UNKNOWN_4
InterPro; IPR001632; -.
InterPro; IPR001680; -.
Pfan, PF00400; WD40; 7.
PRINTS; PR00119; GPROTEINB.
PRINTS; PR00120; GPROTEINB.
PROSITE; PS00678; WD_REPEATS; UN
REPEAT; WD repeat.
SEQUENCE 330 AA; 36329 MW; F
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12;

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